

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:41:23 ; Search time 29.7961 Seconds

(without alignments)
1108.034 Million cell updates/sec

Title: US-09-224-683-46

Perfect score: 1061

Sequence: 1 MKKTQTWLTCIYLQLLFN.....AASLRNDSSSNSKYIYL 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq.19Jun03.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1061	100.0	208	16 AAR83977	Human stem cell fa
2	1061	100.0	208	17 AAR83175	Stem cell factor.
3	1061	100.0	208	21 AAY53286	Human stem cell fa
4	1061	100.0	208	22 AAU05255	Human stem cell fa
5	1061	100.0	208	22 AAB83355	Human stem cell f
6	1061	100.0	208	22 AAU02457	Human SCF (stem ce
7	1061	100.0	208	22 AAU02764	Human SCF (stem ce
8	1061	100.0	208	22 AAB73565	Human SCF (stem ce
9	1061	100.0	208	22 AAB96940	Human stem cell fa

10	1061	100.0	208	23 AAB95641	Human SCF protein
11	1061	100.0	208	23 AAE22323	Human stem cell fa
12	1052	99.2	208	12 AAR11710	Human Stem Cell Fa
13	1030	97.1	273	12 AAR11711	Human Stem Cell Fa
14	1030	97.1	273	13 AAR20647	Human mast cell gr
15	1030	97.1	273	16 AAR83978	Human stem cell fa
16	1030	97.1	273	18 AAW27607	Human recombinant
17	1030	97.1	273	21 AAY53284	Human SCF protein
18	1030	97.1	273	22 AAU05256	Human stem cell fa
19	1030	97.1	273	22 AAU05266	Human SCF protein
20	1030	97.1	273	22 AAB98356	Human stem cell fa
21	1030	97.1	273	22 AAB98357	Human SCF protein
22	1030	97.1	273	22 AAB98367	Human SCF protein
23	1030	97.1	273	22 AAU02458	Human SCF (stem ce
24	1030	97.1	273	22 AAU02460	Human SCF protein
25	1030	97.1	273	22 AAU02765	Human SCF (stem ce
26	1030	97.1	273	22 AAU02766	Human SCF protein
27	1030	97.1	273	22 AAB73566	Human SCF (stem ce
28	1030	97.1	273	22 AAB73567	Human SCF protein
29	1030	97.1	273	22 AAB96941	Human stem cell fa
30	1030	97.1	273	22 AAB96942	Human stem cell fa
31	1030	97.1	273	22 AAB96952	Human stem cell fa
32	1030	97.1	273	23 AAB95642	Human SCF protein
33	1030	97.1	273	23 AAE22324	Human stem cell fa
34	1030	97.1	273	23 AAE22326	Human SCF protein
35	1026	96.7	273	22 AAU05257	Monkey stem cell f
36	1026	96.7	273	22 AAB98358	Monkey SCF protein
37	1026	96.7	273	22 AAU02484	Monkey SCF (stem c
38	1026	96.7	273	22 AAU02770	Monkey SCF (stem c
39	1026	96.7	273	22 AAB73571	Monkey SCF (stem c
40	1026	96.7	273	22 AAB96943	Monkey stem cell f
41	1021	96.2	273	14 AAR32166	hKL fragment A. S
42	1011	95.3	198	23 AAB95640	Human SCF protein
43	1001	94.3	196	22 AAU02456	Human SCF (stem ce
44	1001	94.3	196	22 AAU02763	Human SCF (stem ce
45	1001	94.3	196	22 AAB73564	Human SCF (stem ce

ALIGNMENTS

RESULT 1
AAR83977
ID AAR83977 standard; Protein; 208 AA.
XX AAR83977;
AC AAR83977;
XX
DT 25-MAR-2003 (updated)
DT 14-MAY-1996 (first entry)
XX
DE Human stem cell factor (SCF).
XX
XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow.
XX
XX Homo sapiens.
XX
XX Key
FH Peptide
FT 1..25
FT /label= sig_peptide
FT Protein
FT 26..183
FT /label= mat_peptide
XX
PN EP676470-A1.
XX
PD 11-OCT-1995.
XX
XX
PF 04-OCT-1990; 9SEP-0105391.
XX
XX 01-OCT-1990; 9OUS-0589701.
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 9OUS-0537198.

24-AUG-1990: 90US-0573616.
28-SEP-1990: 90MO-US05548.
(AMGE-) AMGEN INC.
Bosselman RA, Martin FH, Suggs SV, Zsebo KM;
WPI: 1995-346090/45.
N-PSDB: AAT04889.
New stem cell factor polypeptide(s) - for stimulating the growth of
primitive progenitor cells, esp. for treating disorders involving
blood cells
Disclosure; Fig 15C; 127pp; English.
AA83997 is human stem cell factor (SCF). Non-naturally occurring SCF
and C-terminally truncated polypeptides stimulate growth of primitive
progenitors such as hematopoietic progenitor cells, neural stem cells
and primordial germ stem cells. The peptides can be used in a
composition for treating leucopenia, anaemia or thrombocytopenia, for
enhancing engraftment of bone marrow during transplantation or for
bone marrow recovery after chemotherapy or radiation-induced bone
marrow aplasia or myelosuppression. They can also be used for the
treating neoplasia, nerve damage, infertility, intestinal damage or
myeloproliferative disorders. Antibodies may be raised against the
peptides for use in detection or neutralisation of SCF in serum. SCF
may be useful for the treatment of AIDS and severe combined
immunodeficiency (SCID) states alone or in combination with other
factors such as IL-7.
[updated on 25-MAR-2003 to correct PF field.]
Sequence 208 AA;

Query Match	100.0%	Score 1061	DB 16	Length 208
Best local Similarity	100.0%	Pred. No. 4.8e-104		
Matches 208	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MKKTQFWILTCIYLQDLLFNPLVKEGICRRNRVTNNVADYKLVANLPKQYMITLKKVPG	60	
Db	1	MKKTQFWILTCIYLQDLLFNPLVKEGICRRNRVTNNVADYKLVANLPKQYMITLKKVPG	60	
Qy	61	MDVLPSHCWISSEWVQVLSLTDLLDKPSNISSEGLSNYSITDKLVNIYVDLVCECKENSS	120	
Db	61	MDVLPSHCWISSEWVQVLSLTDLLDKPSNISSEGLSNYSITDKLVNIYVDLVCECKENSS	120	
Qy	121	KDILKSFKSPBPLFTPEEFPRIPNRSIDAFKDFVAVSETSDCVVSSITLSPKDSRVSVT	180	
Db	121	KDILKSFKSPBPLFTPEEFPRIPNRSIDAFKDFVAVSETSDCVVSSITLSPKDSRVSVT	180	
Qy	181	KPFMLPPVAASSLRNDSSSSNSKITYLI	208	
Db	181	KPFMLPPVAASSLRNDSSSSNSKITYLI	208	

RESULT 2	AAAR95175	standard; Protein; 208 AA.
XX	AAAR95175:	
AC		
DT	03-OCT-1996 (first entry)	
XX		
DE	Stem cell factor.	
XX		
KM	Stem cell factor; SCF, splice variant; embryo implantation;	
KW	in vitro fertilisation; IVF.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FT	1..25	
FT	/label= Sig_peptide	

FT	Protein	26..208
PT	/label= Mat_protein	
XX		
XX		
PN	W09614410-A1.	
PD		
XX	17-MAY-1996.	
XX		
PF	31-OCT-1995;	95WO-GB02547.
XX		
PR	28-APR-1995;	95GB-0008618.
PR	04-NOV-1994;	94GB-0022293.
XX		
PA	(ISTE) ARS APPLIED RES SYST HOLDING NV.	
XX		
PI	Dellow KA, Sharkey AM, Smith SK;	
XX		
DR	WPJ; 1996-251760/25.	
DR	N-PsDB; AAT29489.	
XX		
PT	Stem cell factor comprising C-terminal sequence given in	
PT	specification - useful to ensure correct development of	
PT	pre-implantation embryos before implantation into subject	
XX		
PS	Disclosure; Fig 2; 25pp: English.	
XX		
CC	A DNA sequence (AAT29489) codes for human stem cell factor (SCF).	
CC	(AAR95175). The full-length SCF transcript consists of 8 exons.	
CC	A novel splice variant has been identified that appears to arise	
CC	from the inclusion of a novel exon (see also AAT29488) between exons	
CC	3 and 4 of the gene. The resulting frameshift produces a novel	
CC	SCF consisting of the first 39 amino acids of mature SCF followed	
CC	by a 33-amino acid C-terminal region (AAR95174). The novel SCF is	
CC	useful for ensuring correct development of pre-implantation embryos.	
XX		
XQ	Sequence 208 AA;	

Query Match	Score	DB	Length
100.0%;	1061;	DB 17;	Length 208;
Best Local Similarity	100.0%;	Pred. No. 4.8e-104;	
Matches 208;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;

Query	1	MKKTQWILTCIYLQLLFNLVKTGICRRNVTNVNDVTKLVANLPEKDYMITLKVYPG	60
Db	1	MKKQTWILTCIYLQLLFNLVKTGICRRNVTNVNDVTKLVANLPEKDYMITLKVYPG	60
Qy	61	MDVLPSCWISSEMYVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS	120
Db	61	MDVLPSCWISSEMYVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS	120
Qy	121	KDLKSKSPKSPRLFTPEEPFRIFNRSIDAKDKVVAASETSDCVVSSTLSPKDSRVSVT	180
Db	121	KDLKSKSPKSPRLFTPEEPFRIFNRSIDAKDKVVAASETSDCVVSSTLSPKDSRVSVT	180
Qy	181	KPFMLPVAASLSLNDSSSSNSKITYIL	208
Db	181	KPFMLPVAASLSLNDSSSSNSKITYIL	208

RESULT 3	ID	AA53286	standard; Protein: 208 AA.
XX	AA53286;		
XX	27-JUL-2000	(first entry)	
XX			
DB			Human stem cell factor protein sequence.
XX			
XX			Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW			primitive progenitor cell; haematopoietic disorder; syngenic;
KW			allogeneic; autologous bone marrow transplant; gene therapy;
KW			transfection; haematopoietic stem cell; acute blood loss; neoplasia;
KW			cancer.
XX			

```

OS Homo sapiens.
XX
XX EP92579-A1.
XX
XX 12-APR-2000.
XX
XX 04-OCT-1990; 99EP-0122861.
XX
XX 16-OCT-1989; 89US-0422383.
XX 11-JUN-1990; 90US-0537198.
XX 24-AUG-1990; 90US-0573616.
XX 28-SEP-1990; 90MO-US05548.
XX 01-OCT-1990; 90US-0589701.
XX 04-OCT-1990; 90EP-0310899.
XX
XX (AMGE-) AMGEN INC.
XX
XX Zsebo KM, Suggs SV, BosseImann RA, Martin FH,
XX
XX WPI; 2000-259135/23.
XX N-PSDB; AAA13716.
XX
XX Production of hematopoietic cells suitable for administration to a
XX subject using progenitor cells and expanding the cells using stem cell
XX factor -
XX
XX Claim 21; Fig 15C; 123pp; English.
XX
XX A method has been developed of making haematopoietic cells suitable for
XX administration to a subject. The method comprises: (a) obtaining
XX haematopoietic progenitor cells from a donor; and (b) expanding the
XX cells by adding to the cells a haematopoietically effective dose of a
XX polypeptide product having at least part of the primary structural
XX confirmation and one or more of the biological properties of naturally
XX occurring stem cell factor (SCF). The method is useful for stimulating
XX primitive progenitor cells including early haematopoietic progenitor
XX cells which are capable of maturing to erythroid, megakaryocyte,
XX granulocyte, lymphocyte and macrophage cells. SCF results in absolute
XX increases in hematopoietic cells of both myeloid and lymphoid lineages.
XX SCF is useful for treating haematopoietic disorders. The method is
XX useful for expanding early haematopoietic progenitors in syngeneic,
XX allogeneic or autologous bone marrow transplant. SCF is useful for
XX enhancing the efficiency of gene therapy based on transfecting
XX haematopoietic stem cells. SCF is also useful for combating the
XX myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
XX haematopoietic recovery after acute blood loss and as a boost to the
XX immune system for fighting neoplasia (cancer). The present sequence
XX represents a specifically claimed human SCF from the present invention.
XX
XX Sequence 208 AA;
XX
XX Query Match 100.0%; Score 1061; DB 21; Length 208;
XX Best Local Similarity 100.0%; Pred. No. 4,8e-104;
XX Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MKKTQWILTCITLQLLFNPLVKTEGICRNVTNNVDVTLVANLPKDWYITLLKYVVG 60
XX
XX 1 MKKTQWILTCITLQLLFNPLVKTEGICRNVTNNVDVTLVANLPKDWYITLLKYVVG 60
XX
XX 61 MDVLPCHCWISEWVQVDSITDLDKFSNISGLSNYSIIDKLVNIIVDLVECVKENSS 120
XX
XX 61 MDVLPCHCWISEWVQVDSITDLDKFSNISGLSNYSIIDKLVNIIVDLVECVKENSS 120
XX
XX 121 KDLKSKFSKSPERLPFTPEEFRIFNRSIDAFKDFVAVASSTSDCVSSSTSPKDSRVSVT 180
XX
XX 121 KDLKSKFSKSPERLPFTPEEFRIFNRSIDAFKDFVAVASSTSDCVSSSTSPKDSRVSVT 180
XX
XX 181 KPFLPVAASSLRNDSSSSSKYIYL 208
XX
XX 181 KPFLPVAASSLRNDSSSSSKYIYL 208
XX
XX RESULT 4

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AAU05255
ID AAU05255 standard; Protein; 208 AA.
XX
XX AC AAU05255;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human stem cell factor (SCF) protein encoded by SCF cDNA.
XX
XX Human, stem cell factor; SCF; haematopoietic progenitor cell;
XX blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
XX hypopigmentation disorder; viral disorder; AIDS.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..25
XX Protein /label= Signal_peptide
XX /label= Mature_SCF
XX
XX US6248319-B1.
XX
XX 19-JUN-2001.
XX
XX 24-MAY-1995; 95US-0449653.
XX
XX 10-APR-1991; 91US-0684535.
XX 25-NOV-1992; 92US-0982255.
XX 16-OCT-1989; 89US-0422383.
XX 11-JUN-1990; 90US-0537198.
XX 24-AUG-1990; 90US-0573616.
XX 01-OCT-1990; 90US-0589701.
XX 21-DEC-1993; 93US-0172325.
XX
XX (ZSEB/) ZSEBO K M.
XX (BOSS/) BOSSELMAN R A.
XX (SUGS/) SUGGS S V.
XX (MART/) MARTIN F H.
XX
XX Zsebo KM, BosseImann RA, Suggs SV, Martin FH;
XX
XX WPI; 2001-407312/43.
XX N-PSDB; AAS10457.
XX
XX Increasing the number of early haematopoietic progenitor cells in the
XX peripheral blood useful for the treatment of blood disorders including
XX Hodgkin's disease comprises the administration of human stem cell
XX factor -
XX
XX Example 3; Fig 15C; 210pp; English.
XX
XX The present sequence represents human stem cell factor (SCF). The
XX sequence is described in an invention relating to novel stem cell
XX factors, the polynucleotides encoding them and methods for producing
XX the stem cell factors. The methods involve increasing the number of
XX early haematopoietic progenitor cells in human peripheral blood by
XX administering a haematopoietically effective human stem cell factor
XX polypeptide. The methods are useful for the treatment of blood
XX disorders, including myelofibrosis, myelocytosis, osteopetrosis,
XX metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
XX disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
XX anaemia, malaria, vitamin B12 and folic acid deficiency,
XX hypopigmentation disorders i.e. prebaldism and viral induced disorders,
XX including AIDS.
XX
XX Sequence 208 AA;
XX
XX Query Match 100.0%; Score 1061; DB 22; Length 208;
XX Best Local Similarity 100.0%; Pred. No. 4,8e-104;
XX Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MKKTQWILTCITLQLLFNPLVKTEGICRNVTNNVDVTLVANLPKDWYITLLKYVVG 60
XX

```

```

Db      1 MKKTQWILTCIYQLLLFNPVLVKTGICRRNVTNNVADVTKLVANLPKDYMITLKYPG 60
Qy      61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISEGLSNYSIIDKLVINIVDVLVECKENSS 120
Db      61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISEGLSNYSIIDKLVINIVDVLVECKENSS 120
Qy      121 KDLKSFSPSPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Db      121 KDLKSFSPSPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Qy      181 KPFLMPVVAASSLRNDSNSSNSKYIYLI 208
Db      181 KPFLMPVVAASSLRNDSNSSNSKYIYLI 208

RESULT 5
AAB98355
ID      AAB98355 standard; Protein; 208 AA.
AC      AAB98355;
XX
XX      21-AUG-2001 (first entry)
DE      Human stem cell factor (SCF) protein SEQ ID NO:46.
XX
XX      Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
XX      gene therapy.
XX      Homo sapiens.
XX      US6207454-B1.
XX      27-MAR-2001.
XX      31-DEC-1998; 98US-0224681.
XX
XX      21-DEC-1993; 93US-0172329.
XX      24-MAY-1995; 95US-0449653.
XX      12-JUN-1998; 98US-0005893.
XX      25-NOV-1992; 92US-0982255.
XX      16-OCT-1989; 89US-0422383.
XX      11-JUN-1990; 90US-0537198.
XX      24-AUG-1990; 90US-0573616.
XX      01-OCT-1990; 90US-0589701.
XX
XX      (AMGE-) AMGEN INC.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX      WPI; 2001-366062/38.
XX      N-PSDB; AAH41341.
XX
XX      Enhancing efficiency of transfer of polynucleotide into a target
XX      mammalian cell in vitro, involves exposing cell that expresses a stem
XX      cell factor receptor to stem cell factor, and introducing
XX      polynucleotide into cell in vitro -
XX
XX      Claim 16; Fig 15C; 210pp; English.
XX
XX      The present invention describes a method for enhancing (E) the
XX      efficiency of transfer of a polynucleotide (I) into a target mammalian
XX      cell (II) in vitro, comprising exposing (II) that expresses a stem cell
XX      factor (SCF) receptor to a biologically active SCF, its analogue or
XX      fragment, which induces cell proliferation, and introducing (I) to (II)
XX      in vitro. Exposure of SCF to (II) results in increased uptake of (I)
XX      into the cell. The method is useful for enhancing the efficiency of the
XX      transfer of a polynucleotide into a target mammalian cell in vitro.
XX      The method is useful in gene therapy techniques. AAH41301 to AAH41364
XX      and AAB98351 to AAB98390 represent sequences used in the exemplification
XX      of the present invention.
XX
XX      Sequence 208 AA:

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Query Match      100.0%; Score 1061; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.8e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MKKTQWILTCIYQLLLFNPVLVKTGICRRNVTNNVADVTKLVANLPKDYMITLKYPG 60
Db      1 MKKTQWILTCIYQLLLFNPVLVKTGICRRNVTNNVADVTKLVANLPKDYMITLKYPG 60
Qy      61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISEGLSNYSIIDKLVINIVDVLVECKENSS 120
Db      61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISEGLSNYSIIDKLVINIVDVLVECKENSS 120
Qy      121 KDLKSFSPSPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Db      121 KDLKSFSPSPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Qy      181 KPFLMPVVAASSLRNDSNSSNSKYIYLI 208
Db      181 KPFLMPVVAASSLRNDSNSSNSKYIYLI 208

RESULT 6
AAU02457
ID      AAU02457 standard; Protein; 208 AA.
XX
XX      AAU02457;
XX
XX      29-AUG-2001 (first entry)
DE      Human SCF (stem cell factor) protein encoded by SCF cDNA.
XX
XX      Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX      blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX      anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      Peptide 1..25 /label= Signal_peptide
XX      Protein 26..208 /label= Mature_SCF
XX
XX      US6207417-B1.
XX
XX      27-MAR-2001.
XX
XX      07-JUN-1995; 95US-0482918.
XX
XX      21-DEC-1993; 93US-0172329.
XX      16-OCT-1989; 89US-0422383.
XX      11-JUN-1990; 90US-0537198.
XX      24-AUG-1990; 90US-0573616.
XX      01-OCT-1990; 90US-0589701.
XX
XX      (ZSEBO/) ZSEBO K M.
XX      (BOSS/) BOSSSELMAN R A.
XX      (SUGG/) SUGGS S V.
XX      (MART/) MARTIN F H.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX      WPI; 2001-298941/31.
XX      N-PSDB; AAS04121.
XX
XX      Novel nucleic acids encoding stem cell factor useful for treating
XX      disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
XX      disease, Kala azar, anaemia and septicemia -
XX      Example 3; Fig 15C; 209pp; English.
XX
XX      The present sequence represents human SCF (stem cell factor) protein

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CC encoded by SCF cDNA. The present invention relates to novel stem cell
 CC factors (AAU02453-AAU02458, AAU02460, AAU02461) and the polynucleotides
 CC encoding them. SCF stimulate primitive progenitor cells including early
 CC haematopoietic progenitor cells. The invention also describes SCF
 CC peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAU04081-AAU04117) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing
 CC SCF and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.

CC Sequence 208 AA;

Query Match 100.0%; Score 1061; DB 22; Length 208;

Best Local Similarity 100.0%; Pred. No. 4.8e-104;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFNPLVKTEGICRNRYTNNAVQVTKLVANLPKDYMITLKYPG 60

DB 1 MKKTQWILTCIYQLLFNPLVKTEGICRNRYTNNAVQVTKLVANLPKDYMITLKYPG 60

QY 61 MDVLPSCWISSEWVQLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDDLVECVKENSS 120

DB 61 MDVLPSCWISSEWVQLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDDLVECVKENSS 120

QY 121 KDLKSFSPKPEPRLFTPEEPFRIFNRSIDAFKDFVAVASSTDCVASTLSPKDSRVSVT 180

DB 121 KDLKSFSPKPEPRLFTPEEPFRIFNRSIDAFKDFVAVASSTDCVASTLSPKDSRVSVT 180

QY 181 KPFMLPPVAASSLRNDSSSSNSKYYILI 208

DB 181 KPFMLPPVAASSLRNDSSSSNSKYYILI 208

RESULT 7

ID AAU02764 standard; Protein; 208 AA.

XX AAU02764;

AC 29-AUG-2001 (first entry)

XX Human SCF (stem cell factor) protein encoded by SCF cDNA.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;

KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= Signal_peptide

FT /label= Mature_SCF

XX US6218148-B1.

XX 17-APR-2001.

XX 21-DEC-1993; 93US-0172329.

XX 25-NOV-1992; 92US-0982255.

XX 16-OCT-1989; 89US-0422383.

XX 11-JUN-1990; 90US-0537198.

XX 24-AUG-1990; 90US-0573616.

XX 01-OCT-1990; 90US-0589701.

PA (AMGE-) AMGEN INC.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

PI WPI; 2001-281051/29.

DR N-PSDB; AAS04222.

XX Isolated DNA sequence, encoding polypeptide product useful for

PT stimulating growth of early haematopoietic progenitor cells -

PS Example 3; Fig 15C; 167bp; English.

XX The present sequence represents human SCF (stem cell factor) protein
 CC encoded by SCF cDNA. The present invention relates to novel stem cell
 CC factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the
 CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
 CC including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
 CC (AAS04182-AAS04218) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing
 CC SCF and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.

XX Sequence 208 AA;

Query Match 100.0%; Score 1061; DB 22; Length 208;

Best Local Similarity 100.0%; Pred. No. 4.8e-104; Indels 0; Gaps 0;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFNPLVKTEGICRNRYTNNAVQVTKLVANLPKDYMITLKYPG 60

DB 1 MKKTQWILTCIYQLLFNPLVKTEGICRNRYTNNAVQVTKLVANLPKDYMITLKYPG 60

QY 61 MDVLPSCWISSEWVQLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDDLVECVKENSS 120

DB 61 MDVLPSCWISSEWVQLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDDLVECVKENSS 120

QY 121 KDLKSFSPKPEPRLFTPEEPFRIFNRSIDAFKDFVAVASSTDCVASTLSPKDSRVSVT 180

DB 121 KDLKSFSPKPEPRLFTPEEPFRIFNRSIDAFKDFVAVASSTDCVASTLSPKDSRVSVT 180

QY 181 KPFMLPPVAASSLRNDSSSSNSKYYILI 208

DB 181 KPFMLPPVAASSLRNDSSSSNSKYYILI 208

RESULT 8

ID AAB73565 standard; Protein; 208 AA.

XX AAB73565;

AC 07-AUG-2001 (first entry)

XX Human SCF (stem cell factor) protein #2, encoded by SCF cDNA.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;

KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= Signal_peptide

FT /label= Mature_SCF

```

XX XX US6204363-B1.
PN XX
XX XX 20-MAR-2001.
PD XX
XX XX 25-NOV-1992; 92US-0982255.
XX XX
XX PR 10-APR-1991; 91US-0684535.
XX PR 16-OCT-1989; 89US-0422383.
XX PR 11-JUN-1990; 90US-0537198.
XX PR 24-AUG-1990; 90US-0573616.
XX PR 01-OCT-1990; 90US-0589701.
XX XX
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX DR WPI; 2001-256683/26.
XX DR N-PSDB; AAH23899.
XX XX
XX PT New stem cell factor polypeptides and their analogs which stimulate
XX PT growth of early hematopoietic progenitors, useful for treating aplastic
XX PT anemia, carcinoma, multiple myeloma, vitiligo, Kala azar, Hodgkin's
XX PT disease -
XX PS Claim 1; Fig 15C; 166pp; English.
XX XX
XX CC The present sequence represents human SCF (stem cell factor) protein
XX CC encoded by SCF cDNA. The present invention relates to novel stem cell
XX CC factors (AAH73561-AAH73568, AAH73571-AAH73576) and the
XX CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX CC including early haematopoietic progenitor cells. The invention also
XX CC describes SCF peptides (AAH73578-AAH73597) and the oligonucleotides
XX CC (AAH23859-AAH23895) used in the isolation of human and rat SCF
XX CC sequences. The polynucleotide encoding SCF is useful for producing
XX CC SCF and useful in gene therapy. It is useful for treating disorders
XX CC involving blood cells such as myelofibrosis, metastatic carcinoma,
XX CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
XX CC sarcoidosis, military tuberculosis, disseminated fungus disease,
XX CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX CC pyridoxine deficiency, and hypopigmentation disorders such as
XX CC piebaldism and vitiligo.
XX CC
XX SQ Sequence 208 AA;
XX
XX Query Match 100.0%; Score 1061; DB 22; Length 208;
XX Best Local Similarity 100.0%; Pred. No. 4,8e-104;
XX Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYVPG 60
XX DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYVPG 60
XX
XX QY 61 MDVLPSCWISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECVKENS 120
XX DB 61 MDVLPSCWISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECVKENS 120
XX
XX QY 121 KDLKSFKSPPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
XX DB 121 KDLKSFKSPPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
XX
XX QY 181 KPFLMPVAASSLRNDSSSNKYIYLI 208
XX DB 181 KPFLMPVAASSLRNDSSSNKYIYLI 208
XX
XX RESULT 9
XX AAB96940
XX ID AAB96940 standard; Protein; 208 AA.
XX AC AAB96940;
XX XX

```

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DT DT 13-JUL-2001 (first entry)
XX XX
XX DE Human stem cell factor SEQ ID NO: 46.
XX XX
XX KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
XX KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
XX KW neurological damage; intestinal damage; infertility; AIDS; SCID;
XX KW severe combined immunodeficiency.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key
XX FH Peptide 1..25
XX FT /label= signal_peptide
XX FT Protein 26..208
XX FT /label= mature_stem_cell_factor
XX XX
XX PN US6207802-B1.
XX PN
XX PD 27-MAR-2001.
XX PD
XX PF 09-NOV-1994; 94US-0336728.
XX PF
XX PR 25-NOV-1992; 92US-0982255.
XX PR 16-OCT-1989; 89US-0422383.
XX PR 11-JUN-1990; 90US-0537198.
XX PR 24-AUG-1990; 90US-0573616.
XX PR 01-OCT-1990; 90US-0589701.
XX PR
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX DR WPI; 2001-353108/37.
XX DR N-PSDB; AAF89101.
XX XX
XX PT Novel isolated non-human mammalian stem cell factor polypeptide
XX PT stimulating growth of early haematopoietic progenitor cells, useful for
XX PT treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
XX PT sarcoidosis -
XX PT
XX PS Disclosure; Fig 15C; 209pp; English.
XX PS
XX CC The present invention provides the protein and coding sequences of
XX CC mammalian stem cell factors (SCFs). These are capable of stimulating the
XX CC growth of early haematopoietic progenitor cells, neural stem cells and
XX CC primordial germ stem cells. The sequences are useful in the treatment of
XX CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
XX CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
XX CC immunodeficiency (SCID). The present sequence is an SCF described in the
XX CC invention.
XX CC
XX SQ Sequence 208 AA;
XX
XX Query Match 100.0%; Score 1061; DB 22; Length 208;
XX Best Local Similarity 100.0%; Pred. No. 4,8e-104;
XX Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYVPG 60
XX DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYVPG 60
XX
XX QY 61 MDVLPSCWISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECVKENS 120
XX DB 61 MDVLPSCWISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECVKENS 120
XX
XX QY 121 KDLKSFKSPPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
XX DB 121 KDLKSFKSPPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
XX
XX QY 181 KPFLMPVAASSLRNDSSSNKYIYLI 208
XX DB 181 KPFLMPVAASSLRNDSSSNKYIYLI 208
XX

```

	D8	161 KPFMLPVAASSLRNDSSSNSTYLLI 208
RESULT 10		
ID ABG95641 standard; Protein; 208 AA.		
XX AC ABG95641;		
XX DT 05-DEC-2002 (first entry)		
XX DE Human SCF protein sequence encoded by cDNA.		
KW Stem cell factor; SCF; blood-forming system; blood cell disorder; KW haematopoietic system; metastatic carcinoma; acute leukaemia; KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo; KM refractory erythroblastic anaemia;iliary tuberculosis; cytostatic; KV disseminated fungus disease;haematopoietic;tuberculousitic; KW antianaemic; antifungal; antimalaria;l dermatological;human. XX XX Homo sapiens. OS PN EPI241258-A2. XX PD 18-SEP-2002. XX PE 04-OCT-1990; 2002EP-0008587. XX PR 16-OCT-1989; 89US-0422383. PR 11-JUN-1980; 90US-0537198. PR 24-AUG-1990; 90US-0573616. PR 28-SEP-1990; 90WO-US05548. PR 01-OCT-1990; 90US-0589701. PR 04-OCT-1990; 90EP-0310899. PR 04-OCT-1990; 95EP-0105391. XX PA (AMGE-) AMGEN INC. PI Zeebo KM, Suggs SV, Bosselman RA, Martin FH; DR MPI; 2002-684093/74. N-PDB; ABS73858. PT Production of a human stem cell factor (SCF) polypeptide for treating disorders involving blood cells, such as leukaemia, comprises culturing mammalian cells comprising non-human SCF promoter DNA linked to DNA encoding the human SCF - PT XX Claim 1; Fig 15C; 120pp; English. PS The present invention relates to novel stem cell factors (SCFs), XX polynucleotide sequences encoding the SCFs, and methods of producing them. SCFs are involved in the blood-forming (haematopoietic) CC system in mammals, particularly humans. The method of the invention CC is useful for the production of human SCF. The stem cell factors are CC useful to treat disorders involving blood cells e.g. metastatic CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, CC lymphoma, refractory erythroblastic anaemia, iiliary tuberculosis, CC disseminated fungus disease,malaria, and vitliligo. The present CC sequence represents human SCF protein. XX SQ Sequence 208 AA: Query Match 100.0%; Score 1061; DB 23; Length 208; Best Local Similarity 100.0%; Pred.No.4.8e+104; Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0 QV 1 MKKTOTWLITCYLYQLLFLNPVLVKKEGLCRNVTVNNVKKVTKLIVANLPKDYMITLKYPVG 60 Db 1 MKKTOTWLITCYLYQLLFLNPVLVKKEGLCRNVTVNNVKKVTKLIVANLPKDYMITLKYPVG 60 GV MDVPDSHCMTISMVVQLSDSLTDLDKFENISBGSNSVIIDLVNIIVDYLVECKENS 120		

D6		61	MDVLPEHCIMSEMWQVQLDSGLTDLDDKRSNISEGSLNYSTIIIDKLVMNIVDLIVLCYENSS	12
Oy		121	KDILKSFKSPERPLFTPEEPFRINRSDIAKFDFVASETSDCVSSTLSPEKORSVT	180
Db		121	KDLKSKFSKPERRLLFTPEEFPFRINRSDIAKDFVASETSDCVSSSTLSPKDRSVYT	180
Oy		181	KPMLPPVAASLRNDSSSNKYLYI	208
Db		181	KPMLPPVAASLRNDSSSNKYLYI	208
			RESULT 11	
AEE22323	ID	AAB22323 standard; Protein; 208 AA.		
XX	AC	AAB22323;		
XX	DT	25-JUL-2002 (first entry)		
XX	DE	Human stem cell factor (SCF) protein #2.		
XX	KM	Human; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;		
XX	KW	anaemia; myelosuppression; nerve damage; myeloproliferative disorder;		
XX	KM	infertility; neoplasia; myelofibrosis; myelocytosis; osteoporosis;		
XX	KW	metastatic carcinoma; acute leukæmia; multiple myeloma; sarcoïdosis;		
XX	KW	Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;		
XX	KW	Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;		
XX	KW	Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;		
XX	KM	dissminated fungus disease; Pulmonary septicaemia; plebaldism; AIDS;		
XX	KM	acquired immune deficiency syndrome; malaria; military tuberculosis;		
XX	KW	pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;		
XX	KM	Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo.		
XX	OS	Homo sapiens.		
XX	XX			
FH	Key	Location/Qualifiers		
FT	Peptide	1..25		
FT	/label=	Signal-peptide		
FT	Protein	26..208		
XX	FT	/note= "Human mature SCF protein"		
PN	US2002018763-A1.			
XX				
PD	14-FEB-2002.			
XX				
PF	12-JAN-1998; 98US-0005243.			
XX				
PR	24-MAY-1995; 95US-0449653.			
XX				
PA	(ZSEB/) ZSEBO K M.			
PA	(BOSS/) BOSSELMAN R A.			
PA	(SUGG/) SUGGS S V.			
PA	(MART/) MARTIN F H.			
PI	Zsebo KM, Bosselman RA, Suggs SV, Martin FH;			
DR	WPI; 2002-350789/38.			
DR	N-PSDB; AAD35474.			
XX				
PT	Novel non-naturally-occurring stem cell factor polypeptide, useful for			
PT	treating leucopenia, thrombocytopenia, anemia and for enhancing			
PT	engraftment of bone marrow during transplantation in a mammal -			
XX				
PS	Claim 9; Fig 15C; 217pp; English.			
XX				
CC	The present invention relates to novel non-naturally-occurring stem cell			
CC	factor (SCF) polypeptides having an amino acid sequence sufficiently			
CC	duplicative of that of naturally-occurring SCF to allow possession of			
CC	hamatopoietic biological activity of naturally occurring SCF. Sequences			
CC	of the invention are useful for treating leucopenia, thrombocytopaenia,			
CC	anaemia and for enhancing bone marrow recovery in treatment of radiation,			
CC	engraftment of bone marrow during transplantation in mammals and chemical			
CC	or chemotherapeutic induced bone marrow aplasia or myelosuppression. They			

CC are also useful for treating acquired immune deficiency in a human, nerve
 CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
 CC damage in a mammal. SCF sequences are useful for preparing biologically
 CC active polymer polypeptide adduct, for enhancing transfection of early
 CC hematopoietic progenitor cells with a gene, and transfer of a gene into
 CC a mammal. They are useful for treating myelofibrosis, myelocytosis,
 CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
 CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
 CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
 CC splenic pancytopenia, disseminated fungus disease, malaria, military
 CC tuberculosis, fulminating septicaemia, pyridoxine deficiency, vitamin
 CC B12 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
 CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
 CC and vitiligo. The present sequence is human SCF protein.

XX Sequence 208 AA;

Query Match 100.0%; Score 1061; DB 23; Length 208;

Best Local Similarity 100.0%; Pred. No. 4.8e-104;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRRVYTNVNDVTKLVANLPKDYMITLKYPVG 60
 DB 1 MKKTQWILTCIYQLLFNPLVKTGICRRVYTNVNDVTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCWISEMVOQLSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 DB 61 MDVLPSCWISEMVOQLSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 QY 121 KDLKSKFSKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 DB 121 KDLKSKFSKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 QY 181 KPFMLPPVAASLRNDSSSSNSKTYITL 208
 DB 181 KPFMLPPVAASLRNDSSSSNSKTYITL 208

RESULT 12

ID AAR11710 standard; Protein; 208 AA.

AC AAR11710;

DT 20-JUN-1991 (first entry)

XX Human Stem Cell Factor.

KW Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= sig_peptide

FT Protein /label= mat_protein

PN EP423980-A.

PD 24-APR-1991.

PF 04-OCT-1990; 90EP-0310899.

PR 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90MO-US05548.

XX (AMGE-) AMGEN INC.

PI Zsebo KM, Suggs SV, Bosseman RA, Martin FH;

XX WPI; 1991-119233/17.

DR N-PSDB; AAQ11540, AAQ11541.

PT New naturally-occurring polypeptide stem cell factor analogues -

PT have hematopoietic biological activity of stem cell factor and

PT are used to treat eg leukopenia, AIDS, nerve damage and

PT infertility

XX Disclosure; Fig 15C; 127pp; English.

XX The SCF has the ability to stimulate growth of primitive

CC progenitors including early hematopoietic progenitor cells and non-

CC hematopoietic stem cells such as neural stem cells and primordial

CC germ stem cells. The product may be used in a pharmaceutical

CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,

CC anaemia, AIDS, neoplasia, nerve damage, infertility and

CC intestinal damage.

CC See also AAR11708, AAQ11509-Q11543.

XX Sequence 208 AA;

Query Match 99.2%; Score 1052; DB 12; Length 208;

Best Local Similarity 99.5%; Pred. No. 4.3e-103;

Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRRVYTNVNDVTKLVANLPKDYMITLKYPVG 60

DB 1 MKKTQWILTCIYQLLFNPLVKTGICRRVYTNVNDVTKLVANLPKDYMITLKYPVG 60

QY 61 MDVLPSCWISEMVOQLSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120

DB 61 MDVLPSCWISEMVOQLSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120

QY 121 KDLKSKFSKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180

DB 121 KDLKSKFSKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180

QY 181 KPFMLPPVAASLRNDSSSSNSKTYITL 208

DB 181 KPFMLPPVAASLRNDSSSSNSKTYITL 208

RESULT 13

ID AAR11711 standard; Protein; 273 AA.

AC AAR11711;

DT 20-JUN-1991 (first entry)

XX Human Stem Cell Factor from HT1080 fibrosarcoma line.

KW Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= sig_peptide

FT Protein /label= mat_protein

PN EP423980-A.

PD 24-APR-1991.

PF 04-OCT-1990; 90EP-0310899.

PR 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KM transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS Homo sapiens.

Key Location/Qualifiers
FH Peptide 1..25
FT /label= sig_peptide
FT 26..248
FT Protein /label= mat_SCF

EP676470-A1.

11-OCT-1995.

04-OCT-1990; 95EP-0105391.

01-OCT-1990; 90US-0589701.

16-OCT-1989; 89US-0422383.

11-JUN-1990; 90US-0537198.

24-AUG-1990; 90US-0573616.

28-SEP-1990; 90WC-US05548.

(AMGE-) AMGEN INC.

Bosselman RA, Martin FH, Suggs SV, Zsebo KM;

WPI: 1995-346090/45.

N-PSDB; AAT04890.

New stem cell factor polypeptide(s) - for stimulating the growth of

primitive progenitor cells, esp. for treating disorders involving

blood cells

Claim 9; Fig 42; 127bp; English.

AAR83978 is a human stem cell factor (SCF) derived from the HT1080

fibrosarcoma cell line. Non-naturally occurring SCF and C-terminally

truncated polypeptides, having amino acid sequences sufficiently

duplicative of naturally occurring SCF, stimulate growth of primitive

progenitors such as haematopoietic progenitor cells, neural stem

cells and primordial germ stem cells. The peptides can be used in a

composition for treating leucopenia, anaemia or thrombocytopenia,

for enhancing engraftment of bone marrow during transplantation or

for bone marrow recovery after chemotherapy or radiation-induced bone

marrow aplasia or myelosuppression. They can also be used for

treating neoplasia, nerve damage, infertility, intestinal damage or

myeloproliferative disorders. Antibodies may be raised against the

peptides for use in detection or neutralisation of SCF in serum. SCF

may be useful for the treatment of AIDS and severe combined

immunodeficiency (SCID) states alone or in combination with other

factors such as IL-7

(Updated on 25-MAR-2003 to correct PF field.)

Sequence 273 AA;

Query Match

Best Local Similarity 97.1%; Score 1030; DB 16; Length 273;

Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MKKTQWILTCIYLQLLFNPLVKEGICRNRYNNVKDVKLVANLPKDYMITLKYVPG 60

1 MKKTQWILTCIYLQLLFNPLVKEGICRNRYNNVKDVKLVANLPKDYMITLKYVPG 60

61 MDVLPSCWISSENVOLSDSLDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120

61 MDVLPSCWISSENVOLSDSLDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120

121 KDLKSKFKSPEPRLFPPEFRIFNRSIDAFKDFVAVASSTDCVSSSTLSPKDSRVSVT 180

121 KDLKSKFKSPEPRLFPPEFRIFNRSIDAFKDFVAVASSTDCVSSSTLSPKDSRVSVT 180

181 KPFMLPPVAASLRNDSSSSNSK 203

DB 181 KPFMLPPVAASLRNDSSSSNSK 203

Search completed: February 5, 2004, 15:05:13
Job time: 30.7961 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:03:24 ; Search time 10.8871 Seconds
(without alignments)
808.360 Million cell updates/sec

Title: US-09-224-683-46
Perfect score: 1061
Sequence: 1 MKKTQWILTCIYLQLLFN.....AASLRNDSSSKYIYL 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

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5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1061	100.0	208	3	US-08-836-252A-6
2	1061	100.0	208	3	US-08-482-918-46
3	1061	100.0	208	3	US-09-224-681-46
4	1061	100.0	208	3	US-08-336-728A-46
5	1030	97.1	273	1	US-08-220-378B-2
6	1030	97.1	273	2	US-08-628-428-9
7	1030	97.1	273	3	US-08-482-918-48
8	1030	97.1	273	3	US-08-482-918-49
9	1030	97.1	273	3	US-08-482-918-61
10	1030	97.1	273	3	US-09-224-681-48
11	1030	97.1	273	3	US-09-224-681-49
12	1030	97.1	273	3	US-09-224-681-61
13	1030	97.1	273	3	US-08-336-728A-48
14	1030	97.1	273	3	US-08-336-728A-49
15	1030	97.1	273	3	US-08-336-728A-61
16	1026	96.7	273	3	US-08-482-918-50
17	1026	96.7	273	3	US-09-224-681-50
18	1026	96.7	273	3	US-08-336-728A-50
19	1001	94.3	424	5	US-08-336-728A-44
20	975	91.9	424	5	PCT-US95-03866-14
21	974	91.8	424	5	PCT-US95-03866-12
22	920	86.7	266	3	US-08-482-918-57
23	920	86.7	266	3	US-09-224-681-57
24	920	86.7	266	3	US-08-336-728A-57
25	898	84.6	248	2	US-08-955-848A-82
26	897.5	84.6	274	3	US-08-336-728A-52
27	896.5	84.5	205	1	US-08-133-979A-4

28	896.5	84.5	205	2	US-08-436-890-4	Sequence 4, Appl
29	896.5	84.5	205	2	US-08-451-213-4	Sequence 4, Appl
30	890	83.9	245	3	US-08-482-918-63	Sequence 63, Appl
31	890	83.9	245	3	US-09-224-681-63	Sequence 63, Appl
32	890	83.9	245	3	US-08-336-728A-63	Sequence 63, Appl
33	884	83.3	271	3	US-08-482-918-52	Sequence 52, Appl
34	884	83.3	271	3	US-09-224-681-52	Sequence 52, Appl
35	880.5	83.0	274	3	US-08-336-728A-53	Sequence 53, Appl
36	875	82.5	273	3	US-08-482-918-53	Sequence 53, Appl
37	875	82.5	273	3	US-09-224-681-53	Sequence 53, Appl
38	865	81.5	195	3	US-08-482-918-44	Sequence 44, Appl
39	865	81.5	195	3	US-09-224-681-44	Sequence 44, Appl
40	862.5	81.3	274	3	US-08-482-918-51	Sequence 51, Appl
41	862.5	81.3	274	3	US-09-224-681-51	Sequence 51, Appl
42	862.5	81.3	274	3	US-08-336-728A-51	Sequence 51, Appl
43	861	81.1	273	3	US-08-482-918-42	Sequence 42, Appl
44	861	81.1	273	3	US-09-224-681-42	Sequence 42, Appl
45	861	81.1	273	3	US-08-336-728A-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-08-836-252A-6
Sequence 6, Application US/08836252A
Patent No. 6177556
GENERAL INFORMATION:
APPLICANT: Sharkey, Andrew M.
APPLICANT: Smith, Stephen K.
TITLE OF INVENTION: HUMAN SCF, A SPLICED VARIANT THERMOF, ITS
TITLE OR INVENTION: PHARMACEUTICAL USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,252A
FILING DATE: 31-JULY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB95/02547
FILING DATE: 31-OCT-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422293.2
FILING DATE: 04-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9508618.7
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: ROBERT W. ESMOND
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0550000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-836-252A-6

Query Match 100.0%; Score 1061; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWMLTCTIYLLFNPLVKTGICRNVYNNVKDVKLVANLPKDYMTTLKXVVG 60
DB 1 MKKTQWMLTCTIYLLFNPLVKTGICRNVYNNVKDVKLVANLPKDYMTTLKXVVG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDLVNIYDDLVCEKENS 120
QY 121 KDLKSKFSPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASLRNDSSSNKXYILI 208
DB 181 KPFLPVAASLRNDSSSNKXYILI 208

RESULT 2

US-08-482-918-46
Sequence 46, Application US/08482918
Patent No. 6207417

GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-46

Query Match 100.0%; Score 1061; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWMLTCTIYLLFNPLVKTGICRNVYNNVKDVKLVANLPKDYMTTLKXVVG 60
DB 1 MKKTQWMLTCTIYLLFNPLVKTGICRNVYNNVKDVKLVANLPKDYMTTLKXVVG 60

QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDLVNIYDDLVCEKENS 120

QY 121 KDLKSKFSPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASLRNDSSSNKXYILI 208
DB 181 KPFLPVAASLRNDSSSNKXYILI 208

RESULT 3

US-09-224-681-46
Sequence 46, Application US/09224681
Patent No. 6207454

GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TRANSFER WITH STEM CELL FACTOR (SCF) POLYPEPTIDE
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:

INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-224-681-46

Query Match 100.0%; Score 1061; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTLCIYQLLFPNPLVKTGICRNRVTNNVQDVTKLVAANLPKQYMTLTKVPG 60
DB 1 MKKTQWTLTLCIYQLLFPNPLVKTGICRNRVTNNVQDVTKLVAANLPKQYMTLTKVPG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVIYVDLVCECKENSS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVIYVDLVCECKENSS 120
QY 121 KDLKSFSPSPRLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPSPRLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNSKITYLI 208
DB 181 KPFLPVAASSLRNDSSSSNSKITYLI 208

RESULT 4

US-08-336-728A-46
Sequence 46, Application US/08336728A
Patent No. 6207802

GENERAL INFORMATION:

APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois

COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.

REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-336-728A-46

Query Match 100.0%; Score 1061; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTLCIYQLLFPNPLVKTGICRNRVTNNVQDVTKLVAANLPKQYMTLTKVPG 60
DB 1 MKKTQWTLTLCIYQLLFPNPLVKTGICRNRVTNNVQDVTKLVAANLPKQYMTLTKVPG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVIYVDLVCECKENSS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVIYVDLVCECKENSS 120
QY 121 KDLKSFSPSPRLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPSPRLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNSKITYLI 208
DB 181 KPFLPVAASSLRNDSSSSNSKITYLI 208

RESULT 5

US-08-220-379B-2
Sequence 2, Application US/08220379B
Patent No. 5525708

GENERAL INFORMATION:

APPLICANT: No. 5525708ka, Karl
APPLICANT: Lobell, Robert B
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
City: New York
STATE: New York

COUNTRY: United States of America
ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,379B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CytoMed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

FEATURE:
NAME/KEY: cleavage site
LOCATION: 164..165
US-08-220-3798-2

Query Match 97.1%; Score 1030; DB 1; Length 273;
Best Local Similarity 99.5%; Pred. No. 4.4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPVG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
QY 121 KDLKSFSPSPRLFTPEEFPRIFNRSIDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSFSPSPRLFTPEEFPRIFNRSIDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASLRNDSSSNRK 203
DB 181 KPFMLPVAASLRNDSSSNRK 203

RESULT 6

US-08-628-428-9
Sequence 9, Application US/08628428
Patent No. 5885962

GENERAL INFORMATION:
APPLICANT: Lu, Hsiang
TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,428
FILING DATE: 05-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Knight, Matthew W
REGISTRATION NUMBER: 36,946
REFERENCE/DOCKET NUMBER: A-400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..273
OTHER INFORMATION: /note="NOTE: Mature full length
OTHER INFORMATION: 1-248 SCF protein begins at amino acid 26; amino acid 1-25
OTHER INFORMATION: include Met and leader sequences for membrane band form of hu
OTHER INFORMATION: recombinant SCF."
US-08-628-428-9

Query Match 97.1%; Score 1030; DB 2; Length 273;
Best Local Similarity 99.5%; Pred. No. 4.4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPVG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
QY 121 KDLKSFSPSPRLFTPEEFPRIFNRSIDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSFSPSPRLFTPEEFPRIFNRSIDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASLRNDSSSNRK 203
DB 181 KPFMLPVAASLRNDSSSNRK 203

RESULT 7

US-08-482-918-48
Sequence 48, Application US/08482918
Patent No. 6207417

GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-48

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4.4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPVG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120

Qy	121	KDLKKSRSSEPLFLFPEEFPRIFNNSIAFKD	PVAASETSDCVVSSSTLSEKDSRVSVT	180
Db	121	KDLKKSRSSEPLFLFPEEFPRIFNNSIDAFKD	PVAASETSDCVVSSSTLSEKDSRVSVT	180
Qy	181	KPFMLPVAASSLRANDSSSNRK	203	
Db	181	KPFMLPVAASSLRANDSSSNRK	203	

RESULT 8

US-08-482-918-49
Sequence 49, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zsebo, Krietzina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Sugus, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3886
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-49

Query Match	Match Similarity	97.1% Beat Local	99.5% Conservative	Score 1030	DB 3	Length 273
Matches	202	0	Mismatches 1	Indels	0	Gaps 0
QY	1	MKKTOTWILITCIYLOLLFNPLVKTGTCIRNRVTNNVAKDTLVANLPKDYMITLKYPG	60			
Db	1	MKKTOTWILITCIYLOLLFNPLVKTGTCIRNRVTNNVADTKLVANLPKDYMITLKYPG	60			
QY	61	MDVLPSCMISEMNVQVQLSDSLTDLDLDFKSNISSEGLSNYSIIDKLVNIYDDLVECKENSS	120			
Db	61	MDVLPSCMISEMNVQVQLSDSLTDLDLDFKSNISEGLSNYSIIDKLVNIYDDLVECKENSS	120			
QY	121	KDLKTSFKSPPEERLFTPEEFPRIFENRSIDAFKDFVVAESTSDCVVSSITLSEPKDSRVAVT	180			
Db	121	KDLKTSFKSPPEERLFTPEEFPRIFENRSIDAFKDFVVAESTSDCVVSSITLSEPKDSRVAVT	180			
QY	181	KPFMLPVAASLSLRDSSSSNRK	203			
Db	181	KPFMLPVAASLSLRDSSSSNRK	203			

RESULT 9
ITS-08-48

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US-08-482-918-61
: Sequence 61, Application US/08482918
: Patent No. 6207417
:
: GENERAL INFORMATION:
: APPLICANT: Zsebo, Kriesztina M.
: APPLICANT: Bosselman, Robert A.
: APPLICANT: Suggs, Sidney V.
: APPLICANT: Martin, Francis H.
: TITLE OF INVENTION: Stem Cell Factor
: NUMBER OF SEQUENCES: 104
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/482,918
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Clough, David W.
: REGISTRATION NUMBER: 36,107
: REFERENCE/DOCKET NUMBER: 01017/33005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
:
: TELEX: 25-3856
:
: INFORMATION FOR SEQ ID NO: 61:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 273 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
US-08-482-918-61

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	Query Match	97.1%	Score 1030	DB 3	Length 273
	Best Local Similarity	99.5%	Pred. No. 4,4e-98		
	Matches	Conservative	0	Mismatches 1	Indels 0
				Gaps	0
Qy	1	MKKQTWILITCIYLQLLFNPLVKTGICRRNRVTNNKVDYTKLVANLPKDYMITLKYVPG	60		
Db	1	MKKTQWILITCIYLQLLFNPLVKTGICRRNRVTNNKVDYTKLVANLPKDYMITLKYVPG	60		
Qy	61	MDVLPSHCWISMMVQVSDSLTDLLDKRSNISEGLSNYSIIDKLKYNIVDVLVCEYKENS	120		
Db	61	MDVLPSHCWISMMVQVSDSLTDLLDKRSNISEGLSNYSIIDKLKYNIVDVLVCEYKENS	120		
Qy	121	KDLKSKFSKPEPRLLFTPEEFRIENRSIDAEKDFVVASETSDCVASSTLSPEKDSRVSYT	180		
Db	121	KDLKSKFSKPEPRLLFTPEEFRIENRSIDAEKDFVVASETSDCVASSTLSPEKDSRVSYT	180		
Qy	181	KPEMLPPEVAASLRNDSSSSNK	203		
Db	181	KPEMLPPEVAASLRNDSSSSNK	203		

RESULT 10

US-09-224-661-48
; Sequence 48, Application US/092246681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
; APPLICANT: Bosselmann, Robert A.
; APPLICANT: Suggs, Sidney V.

APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4,4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLLQLLFNPLVKTGICRNRYNNVKQVTKLVANLPKQWITLKTVYG 60
DB 1 MKKTQWILTCIYLLQLLFNPLVKTGICRNRYNNVKQVTKLVANLPKQWITLKTVYG 60
QY 61 MDVLPSCWISSENVVQSLTDLDKFNISSEGLSNYSIIDKLVNIYVDLVECVENSS 120
DB 61 MDVLPSCWISSENVVQSLTDLDKFNISSEGLSNYSIIDKLVNIYVDLVECVENSS 120
QY 121 KDKKSFKSPERPLFTPEEPFRINRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDKKSFKSPERPLFTPEEPFRINRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180

DB 121 KDKKSFKSPERPLFTPEEPFRINRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSSNSK 203
DB 181 KPFMLPVAASSLRNDSSSSNSK 203

RESULT 11
US-09-224-681-49
Sequence 49, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseleman, Robert A.
APPLICANT: Suggey, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-224-681-49

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4,4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPVLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYLQLLFNPVLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEWVQSLDSDLTDLPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSLDSDLTDLPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
QY 121 KDLKSFSPSPRLPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 180
DB 121 KDLKSFSPSPRLPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 180
QY 181 KPFLPVAASSLRNDSSSSSNK 203
DB 181 KPFLPVAASSLRNDSSSSSNK 203

RESULT 12

US-09-224-681-61
Sequence 61, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 0101/735199

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX:

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-224-681-61

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4,4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPVLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYLQLLFNPVLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEWVQSLDSDLTDLPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSLDSDLTDLPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
QY 121 KDLKSFSPSPRLPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 180
DB 121 KDLKSFSPSPRLPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 180
QY 181 KPFLPVAASSLRNDSSSSSNK 203
DB 181 KPFLPVAASSLRNDSSSSSNK 203

RESULT 13

US-08-336-728A-48
Sequence 48, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616

FILED DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-48

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4.4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVDYTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVDYTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDDVECKENSS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDDVECKENSS 120
QY 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSSNSK 203
DB 181 KPFMLPVAASSLRNDSSSSNSK 203

RESULT 14

US-08-336-728A-49
Sequence 49, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255

FILED DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-49

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4.4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVDYTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVDYTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDDVECKENSS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDDVECKENSS 120
QY 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSSNSK 203
DB 181 KPFMLPVAASSLRNDSSSSNSK 203

RESULT 15

US-08-336-728A-61
Sequence 61, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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1      SOFTWARE: Patentin Release #1.0, Version #1.30
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3      CURRENT APPLICATION DATA:
4      APPLICATION NUMBER: US/08/336,728A
5
6      FILING DATE: 09-NOV-1994
7
8      CLASSIFICATION: 424
9
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER: 07/982,255
12
13     FILING DATE: 25-NOV-1992
14
15     PRIOR APPLICATION DATA:
16     APPLICATION NUMBER: 07/589,701
17
18     FILING DATE: 01-OCT-1990
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20     PRIOR APPLICATION DATA:
21     APPLICATION NUMBER: 07/573,616
22
23     FILING DATE: 24-AUG-1990
24
25     PRIOR APPLICATION DATA:
26     APPLICATION NUMBER: 07/537,198
27
28     FILING DATE: 11-JUN-1990
29
30     PRIOR APPLICATION DATA:
31     APPLICATION NUMBER: 07/422,383
32
33     FILING DATE: 16-OCT-1989
34
35     ATTORNEY/AGENT INFORMATION:
36     NAME: Clough, David W.
37
38     REGISTRATION NUMBER: 36,107
39
40     REFERENCE/DOCKET NUMBER: 01017/32956
41
42     TELECOMMUNICATION INFORMATION:
43     TELEPHONE: 312/474-6300
44
45     TELEFAX: 312/474-0448
46
47     TELEX: 25-3856
48
49     INFORMATION FOR SEQ ID NO: 61:
50
51     SEQUENCE CHARACTERISTICS:
52     LENGTH: 273 amino acids
53     TYPE: amino acid
54     TOPOLOGY: linear
55
56     MOLECULE TYPE: protein
57
58     US-08-336-728A-61

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Query Match	97.1%	Score 1030	DB 3	length 273
Best Local Similarity	99.5%	Pred No. 4.4e-98		
Matches 202	Conservative 0	Mismatches 1	Indels 0	Gaps 0

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Db	1	MKTQWMLTLCIYLQLLFNPLVKTGEGIRNVTNNVADVTGLVANI PKDYMILTKVPG	60
Qy	61	MDVLP SHCWI SEMVVO L D S L T D L D K F S N I S E G L S N Y S I I D K L V N I V D D L V E C K E N S S	120
Db	61	MDVLP SHCWI SEMVVO L D S L T D L D K F S N I S E G L S N Y S I I D K L V N I V D D L V E C K E N S S	120
Qy	121	KD L K S K S K S E P P L F P P E E F F R I F N R S I D A F K D P V V A S E T S D C V S S T L S P E K D S R V S V T	180
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Qy	181	K P F M L P P V A A S L R N D S S S S N S K	203
Db	181	K P F M L P P V A A S L R N D S S S S N S K	203

Search completed: February 5, 2004, 15:12:22
Job time : 10.8871 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2004, 15:07:35 / Search time 23.2066 Seconds
(without alignments)
1876.686 Million cell updates/sec

Title: US-09-224-683-46

Perfect score: 1061

Sequence: 1 MKKTQTWLTCTIYQLLEFN.....AASSLRNDSSSSKXYILI 208

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1061	100.0	208	9	US-09-005-243-46 Sequence 46, Appl
2	1061	100.0	208	9	US-09-224-683-46 Sequence 46, Appl
3	1030	97.1	273	9	US-09-005-243-48 Sequence 48, Appl
4	1030	97.1	273	9	US-09-005-243-49 Sequence 49, Appl
5	1030	97.1	273	9	US-09-005-243-61 Sequence 48, Appl
6	1030	97.1	273	9	US-09-224-683-48 Sequence 49, Appl
7	1030	97.1	273	9	US-09-224-683-49 Sequence 49, Appl
8	1030	97.1	273	9	US-09-224-683-61 Sequence 61, Appl
9	1026	96.7	273	9	US-09-005-243-50 Sequence 50, Appl
10	1026	96.7	273	9	US-09-224-683-50 Sequence 50, Appl
11	920	86.7	266	9	US-09-005-243-57 Sequence 57, Appl
12	920	86.7	266	9	US-09-224-683-57 Sequence 57, Appl
13	890	83.9	245	9	US-09-005-243-63 Sequence 63, Appl
14	890	83.9	245	9	US-09-224-683-63 Sequence 63, Appl
15	884	83.3	271	9	US-09-005-243-52 Sequence 52, Appl

16	884	83.3	271	9	US-09-224-683-52	Sequence 52, Appl
17	875	82.5	273	9	US-09-005-243-53	Sequence 53, Appl
18	875	82.5	273	9	US-09-224-683-53	Sequence 53, Appl
19	865	81.5	195	9	US-09-005-243-44	Sequence 44, Appl
20	865	81.5	195	9	US-09-224-683-44	Sequence 44, Appl
21	862.5	81.3	274	9	US-09-005-243-51	Sequence 51, Appl
22	862.5	81.3	274	9	US-09-224-683-51	Sequence 51, Appl
23	861	81.1	273	9	US-09-005-243-42	Sequence 42, Appl
24	861	81.1	273	9	US-09-224-683-42	Sequence 42, Appl
25	855	80.6	273	9	US-09-005-243-55	Sequence 55, Appl
26	855	80.6	273	9	US-09-224-683-55	Sequence 55, Appl
27	855	80.6	273	15	US-10-132-345-4	Sequence 4, Appl
28	854	80.5	273	9	US-09-005-243-54	Sequence 54, Appl
29	854	80.5	273	9	US-09-224-683-54	Sequence 54, Appl
30	843	79.5	166	9	US-09-748-592-2	Sequence 2, Appl
31	839	79.1	164	10	US-09-903-327A-10	Sequence 10, Appl
32	839	79.1	165	12	US-10-320-231A-25	Sequence 25, Appl
33	839	79.1	165	15	US-10-053-355A-2	Sequence 2, Appl
34	839	79.1	393	15	US-10-270-555-1	Sequence 1, Appl
35	837	78.9	613	10	US-09-903-327A-14	Sequence 14, Appl
36	826	77.9	196	9	US-09-005-243-40	Sequence 40, Appl
37	826	77.9	196	9	US-09-224-683-40	Sequence 40, Appl
38	794	74.8	270	15	US-10-132-345-2	Sequence 2, Appl
39	679	64.0	165	9	US-09-005-243-1	Sequence 1, Appl
40	679	64.0	165	9	US-09-224-683-1	Sequence 1, Appl
41	667	62.9	393	15	US-10-270-555-2	Sequence 2, Appl
42	542.5	51.1	282	9	US-09-005-243-56	Sequence 56, Appl
43	542.5	51.1	282	9	US-09-224-683-56	Sequence 56, Appl
44	346	32.6	82	9	US-09-005-243-59	Sequence 59, Appl
45	346	32.6	82	9	US-09-224-683-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-005-243-46
Sequence 46, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-46

Query Match 100.0%; Score 1061; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.9e-96;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLITCIYLLFNPLVKTGICRRNVTNNVADVTYKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWTLITCIYLLFNPLVKTGICRRNVTNNVADVTYKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMVVQLSDSLTDLDPKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
DB 61 MDVLPSCWISSEMVVQLSDSLTDLDPKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
QY 121 KDLKSFSPERPLFTPEEFRIENRSDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIENRSDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208
DB 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208

RESULT 2
US-09-224-683-46
Sequence 46, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-46

Query Match 100.0%; Score 1061; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.9e-96;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLITCIYLLFNPLVKTGICRRNVTNNVADVTYKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWTLITCIYLLFNPLVKTGICRRNVTNNVADVTYKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMVVQLSDSLTDLDPKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
DB 61 MDVLPSCWISSEMVVQLSDSLTDLDPKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
QY 121 KDLKSFSPERPLFTPEEFRIENRSDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIENRSDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208
DB 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208

RESULT 3
US-09-005-243-48
Sequence 48, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-48

Query Match 97.1%; Score 1030; DB 9; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-92;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVTGLVANI PKDYMILTKYVG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVTGLVANI PKDYMILTKYVG 60
QY 61 MDVLPBHCWISSEWVQLSDSLTDLDFKFSNISSEGLSNYSIIDKL VNIYDDLVCEKENS 120
DB 61 MDVLPBHCWISSEWVQLSDSLTDLDFKFSNISSEGLSNYSIIDKL VNIYDDLVCEKENS 120
QY 121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFLMPPVAAASLRNDSSSSNSK 203
DB 181 KPFLMPPVAAASLRNDSSSSNSK 203

RESULT 4
US-09-005-243-49
Sequence 49, Application US/09005243
Patent No. US20020018763A1

GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseleman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6100 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-49

Query Match 97.1%; Score 1030; DB 9; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-92;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVTGLVANI PKDYMILTKYVG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVTGLVANI PKDYMILTKYVG 60
QY 61 MDVLPBHCWISSEWVQLSDSLTDLDFKFSNISSEGLSNYSIIDKL VNIYDDLVCEKENS 120
DB 61 MDVLPBHCWISSEWVQLSDSLTDLDFKFSNISSEGLSNYSIIDKL VNIYDDLVCEKENS 120
QY 121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180

Db 121 KOLKSFSPERLFTPEEPFRIFNRSIDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNSK 203
Db 181 KPFLPVAASSLRNDSSSSNSK 203

RESULT 5

US-09-005-243-61
Sequence 61, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-61

Query Match 97.1%; Score 1030; DB 9; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-92;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNKVTNNVXDVTQLVANLPDQWITLKYPG 60
Db 1 MKKTQWILTCIYQLLLFNPLVKTGICRNKVTNNVXDVTQLVANLPDQWITLKYPG 60
QY 61 MDVLPSCWISPMVQLSDSLTDLLDKPSNISEGISNTSIIDKLVNIYDDLVECYKENS 120
Db 61 MDVLPSCWISPMVQLSDSLTDLLDKPSNISEGISNTSIIDKLVNIYDDLVECYKENS 120
QY 121 KOLKSFSPERLFTPEEPFRIFNRSIDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
Db 121 KOLKSFSPERLFTPEEPFRIFNRSIDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNSK 203
Db 181 KPFLPVAASSLRNDSSSSNSK 203

RESULT 6

US-09-224-683-48
Sequence 48, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-48

Query Match 97.1%; Score 1030; DB 9; Length 273;
Best Local Similarity 99.5%; Pred. No. 1,1e-92;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVDYTKLVANLPKDYMTLLKYVVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVDYTKLVANLPKDYMTLLKYVVG 60
QY 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
QY 121 KDLKSKFSKPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSKPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLMPVAASSLRNDSSSSNSK 203
DB 181 KPFLMPVAASSLRNDSSSSNSK 203

RESULT 7

US-09-224-683-49

Sequence 49, Application US/09224683

Patent No. US20020031491A1

GENERAL INFORMATION:

APPLICANT: Zeebo, Kristina M.

APPLICANT: Bosselman, Robert A.

APPLICANT: Suggs, Sidney V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/224,683

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,893

FILING DATE: 12-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/449,653

FILING DATE: 24-MAY-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/982,255

FILING DATE: 25-NOV-1992

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/589,701

FILING DATE: 01-OCT-1990

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/589,701

FILING DATE: 01-OCT-1990

APPLICATION NUMBER: 07/573,616

FILING DATE: 24-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/537,198

FILING DATE: 11-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 01017/35136

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-224-683-49

Query Match 97.1%; Score 1030; DB 9; Length 273;
Best Local Similarity 99.5%; Pred. No. 1,1e-92;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVDYTKLVANLPKDYMTLLKYVVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVDYTKLVANLPKDYMTLLKYVVG 60
QY 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
QY 121 KDLKSKFSKPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSKPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLMPVAASSLRNDSSSSNSK 203
DB 181 KPFLMPVAASSLRNDSSSSNSK 203

RESULT 8

US-09-224-683-61

Sequence 61, Application US/09224683

Patent No. US20020031491A1

GENERAL INFORMATION:

APPLICANT: Zeebo, Kristina M.

APPLICANT: Bosselman, Robert A.

APPLICANT: Suggs, Sidney V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/224,683

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/449,653
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA: 07/982,255
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA: 07/589,701
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA: 07/573,616
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA: 07/537,198
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA: 07/422,383
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-61

Query Match 97.1%; Score 1030; DB 9; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-92;

Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLNFPLVKTGICRNRVTNNVQDVKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWTLTCTIYQLLNFPLVKTGICRNRVTNNVQDVKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIYDVLVECKENSS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIYDVLVECKENSS 120
QY 121 KDLKSPKSPRPLFTPEEPFRIFNRSIDAFKDFVAVASSETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSPKSPRPLFTPEEPFRIFNRSIDAFKDFVAVASSETSDCVVSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSSNSK 203
DB 181 KPFMLPVAASSLRNDSSSSNSK 203

RESULT 9

US-09-005-243-50
Sequence 50, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristelina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA: 07/589,701
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA: 07/573,616
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA: 07/537,198
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-50

Query Match 96.7%; Score 1026; DB 9; Length 273;
Best Local Similarity 99.0%; Pred. No. 2.7e-92;

Matches 201; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLNFPLVKTGICRNRVTNNVQDVKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWTLTCTIYQLLNFPLVKTGICRNRVTNNVQDVKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIYDVLVECKENSS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIYDVLVECKENSS 120
QY 121 KDLKSPKSPRPLFTPEEPFRIFNRSIDAFKDFVAVASSETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSPKSPRPLFTPEEPFRIFNRSIDAFKDFVAVASSETSDCVVSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSSNSK 203
DB 181 KPFMLPVAASSLRNDSSSSNSK 203

RESULT 10

US-09-224-683-50

Sequence 50, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-50

Query Match 96.7%; Score 1026; DB 9; Length 273;
Best local Similarity 99.0%; Pred. No. 2,7e-92;
Matches 201; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKTQTVWILTCIYQLILFNPVKTGICNRVTNNVKDVTKLVANIPKDYMITTLKYVPG 60
DB 1 MKTQTVWILTCIYQLILFNPVKTGICNRVTNNVKDVTKLVANIPKDYMITTLKYVPG 60

QY 61 MDVLPSCWISBMVQVLSLTDLDKFSNISEGLSNYSIIDKLVINIVDVLVECVKENS 120
DB 61 MDVLPSCWISBMVQVLSLTDLDKFSNISEGLSNYSIIDKLVINIVDVLVECVKENS 120
QY 121 KDLKSFSPSPRLFTPEEFRIENRSDARKDFVVASETSDCVVSTLSPEKDSRVST 180
DB 121 KDLKSFSPSPRLFTPEEFRIENRSDARKDFVVASETSDCVVSTLSPEKDSRVST 180
QY 181 KPFMLPVAASSLRNDSSSSNSK 203
DB 181 KPFMLPVAASSLRNDSSSSNSK 203

RESULT 11
US-09-005-243-57
Sequence 57, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-005-243-57
Query Match
Best Local Similarity 92.6%; Score 920; DB 9; Length 266;
Matches 188; Conservative 7; Mismatches 4; Indels 4; Gaps 4;
QY 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRNRVTNNVKDVTKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWTLTCTIYQLLFPNPLVKT-GICNRVT-DVKDVTKLVANLPKDYMTTLKYVPG 58
QY 61 MDVLPSCWISSEWVQSLTDLDFKFSNISGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 59 MDVLPSCWISSEWVQSLTDLDFKFSNISGLSNYSIIDKLVNIYVDLVECKENSS 117
QY 121 KDLKSKFSPEPRLTPEEPFRIFNRSIDAFKDFVASETDCVSSSTLSEKDSRVSVT 180
DB 118 KNVKKS-KSPEPRLTPEEPFRIFNRSIDAFKDFVASETDCVSSSTLSEKDSRVSVT 176
QY 181 KPFMLPVAASSLRNDSSSSNSK 203
DB 177 KPFMLPVAASSLRNDSSSSNSK 199
RESULT 12
US-09-224-683-57
Sequence 57, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-0448
TELEFAX: 312/474-6300
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-57
Query Match
Best Local Similarity 92.6%; Score 920; DB 9; Length 266;
Matches 188; Conservative 7; Mismatches 4; Indels 4; Gaps 4;
QY 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRNRVTNNVKDVTKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWTLTCTIYQLLFPNPLVKT-GICNRVT-DVKDVTKLVANLPKDYMTTLKYVPG 58
QY 61 MDVLPSCWISSEWVQSLTDLDFKFSNISGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 59 MDVLPSCWISSEWVQSLTDLDFKFSNISGLSNYSIIDKLVNIYVDLVECKENSS 117
QY 121 KDLKSKFSPEPRLTPEEPFRIFNRSIDAFKDFVASETDCVSSSTLSEKDSRVSVT 180
DB 118 KNVKKS-KSPEPRLTPEEPFRIFNRSIDAFKDFVASETDCVSSSTLSEKDSRVSVT 176
QY 181 KPFMLPVAASSLRNDSSSSNSK 203
DB 177 KPFMLPVAASSLRNDSSSSNSK 199
RESULT 13
US-09-005-243-63
Sequence 63, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-63

Query Match 83.9%; Score 890; DB 9; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.9e-79;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVLTGICRNVTNNVKDVTXVANI.PKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLEFNPVLTGICRNVTNNVKDVTXVANI.PKDYMITLKYPG 60
QY 61 MDVLPBHCWISSEWVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVINI.VDVLVECVKENS 120
DB 61 MDVLPBHCWISSEWVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVINI.VDVLVECVKENS 120
QY 121 KDILKSKFSPERPLFTPEEFRI.FNRSIDAFKDFVVASETSDCVSSTISPEK 173
DB 121 KDILKSKFSPERPLFTPEEFRI.FNRSIDAFKDFVVASETSDCVSSTISPEK 173

RESULT 14
US-09-224-683-63
Sequence 63, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristztina M.
APPLICANT: Bosseelman, Robert A.
APPLICANT: Sugan, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-63

Query Match 83.9%; Score 890; DB 9; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.9e-79;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVLTGICRNVTNNVKDVTXVANI.PKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLEFNPVLTGICRNVTNNVKDVTXVANI.PKDYMITLKYPG 60
QY 61 MDVLPBHCWISSEWVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVINI.VDVLVECVKENS 120
DB 61 MDVLPBHCWISSEWVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVINI.VDVLVECVKENS 120
QY 121 KDILKSKFSPERPLFTPEEFRI.FNRSIDAFKDFVVASETSDCVSSTISPEK 173
DB 121 KDILKSKFSPERPLFTPEEFRI.FNRSIDAFKDFVVASETSDCVSSTISPEK 173

RESULT 15
US-09-005-243-52
Sequence 52, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristztina M.
APPLICANT: Bosseelman, Robert A.
APPLICANT: Sugan, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:00:43 ; Search time 11.7466 Seconds
(without alignments)
1702.889 Million cell updates/sec

Title: US-09-224-683-46

Perfect score: 1061
Sequence: 1 MKKTQWILTCIYLQLLFN.....AASLNDSSSSNSKYIYL 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1030	97.1	273	A35974	mast cell growth f
2	899.5	84.8	274	I46575	c-kit ligand - pig
3	890	83.9	245	B61190	mast cell growth f
4	886.5	83.6	274	S47571	stem cell factor,
5	885.5	83.5	202	S58313	stem cell factor p
6	862.5	81.3	274	I46929	stem cell factor -
7	857	80.8	201	B35974	stem cell factor p
8	855	80.6	273	S65801	mast cell growth f
9	715	67.4	245	A37934	mast cell growth f
10	576.5	54.3	124	S29052	stem cell factor -
11	570.5	53.8	287	S70366	stem cell factor 1
12	562.5	53.0	287	S70367	stem cell factor p
13	479.5	45.2	253	S70367	stem cell factor p
14	175.5	16.5	51	B35971	mast cell growth f
15	172.5	16.3	49	A35971	mast cell growth f
16	97.5	9.2	1447	T16086	hypothetical prote
17	97	9.1	1447	F82909	hypothetical prote
18	94	8.9	1293	T27886	hypothetical prote
19	94	8.9	1813	T19295	hypothetical prote
20	92.5	8.7	164	B69616	cell-division init
21	92.5	8.7	512	S68773	citrate (pro-3S)-1
22	92	8.7	935	S63261	SEC21 protein - ye
23	91	8.6	1107	S61667	probable membrane
24	90.5	8.5	616	A69136	ATP-dependent Clp
25	89	8.4	1734	A41101	phospho ester-bind
26	88.5	8.3	545	B44054	orf2 protein - Jun
27	88.5	8.3	941	H84855	phosphoenolpyruvat
28	88	8.3	335	S44922	K18 antigen - Bnta
29	88	8.3	465	H97165	flagellar hook-len

30	88	8.3	702	P97352	membrane-associate
31	88	8.3	1690	T31670	DNA-directed RNA p
32	87.5	8.2	649	T04005	probable protein k
33	87.5	8.2	966	S26235	phosphoenolpyruvat
34	87	8.2	664	T16411	hypothetical prote
35	86.5	8.2	246	T19850	hypothetical prote
36	86.5	8.2	436	F86486	protein F28J9.3 (I
37	86.5	8.2	844	S61104	BRO1 protein - Yea
38	86.5	8.2	1271	T08607	hypothetical prote
39	86	8.1	246	A64579	molybdenum ABC tra
40	86	8.1	496	G86887	threonine synthase
41	86	8.1	660	T22794	hypothetical prote
42	86	8.1	1334	T19493	hypothetical prote
43	85.5	8.1	222	T29762	hypothetical prote
44	85.5	8.1	614	B6461	probable protein k
45	85.5	8.1	636	A45949	mezozoite surface

ALIGNMENTS

RESULT 1

A35974
mast cell growth factor precursor - human
N:Alternate names: kit ligand; stem cell factor
C:Species: Homo sapiens (man)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C/Accession: A35974; A61190
S:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.I
s, J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wrych, J.; Sachdev, I
Cell 63, 203-211, 1990
A>Title: Primary structure and functional expression of rat and human stem cell factor 1
A:Reference number: A35974; MUID:91004219; PMID:2208279
A/Accession: A35974
A/Molecule type: mRNA
A:Residues: 1-273 <MAR>
A/Cross-references: GB:M59964; NID:G37933; PIDN:AAA85450.1; PID:G37934
R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Camizaro, J
Cell Growth Differ. 2, 373-378, 1991
A>Title: Alternative splicing of mRNAs encoding human mast cell growth factor and localiza
A:Reference number: A61190; MUID:92172791; PMID:1724381
A/Accession: A61190
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A:Residues: 1-273 <AND>
A/Genetics:
C/Genetics:
A/Map position: 12q22-12q22
A/Cross-references: GDB:128026; OMIM:184745
C/Suprafamily: mouse mast cell growth factor
C/Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane prote
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-273/Product: mast cell growth factor #status predicted <MCS>
F:26-189/Product: (or 26-190) mast cell growth factor, soluble form #status predicted <I
F:215-237/Domain: transmembrane #status predicted <TM>
F:90,97,118,145,195/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 97.1%; Score 1030; DB 2; Length 273;

Best Local Similarity 99.5%; Pred. No. 4.3e-75;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNVKQVTLVNLPRQVWITLKYPVG	60
DB	1	MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNVKQVTLVNLPRQVWITLKYPVG	60
QY	61	MDVLPSCWISSEWVQSLTDLDFSNISEGLSNYSIIDKLVTIVVDLVECVENSS	120
DB	61	MDVLPSCWISSEWVQSLTDLDFSNISEGLSNYSIIDKLVTIVVDLVECVENSS	120
QY	121	KDLKSKFSPERPLFTPEEFRIFNRSIDAFQDVVASTSCVVSSTLSPKDSRVYT	180
DB	121	KDLKSKFSPERPLFTPEEFRIFNRSIDAFQDVVASTSCVVSSTLSPKDSRVYT	180

QY 181 KPFPMLPPVAASSLRNDSSSSNSK 203
 Db 181 KPFPMLPPVAASSLRNDSSSSNSK 203

RESULT 2

146575
 c-kit ligand - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
 C:Accession: I46575
 R:Zhang, Z.; Anthony, R.V.
 Biol. Reprod. 50, 95-102, 1994
 A:Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization
 A:Reference number: I46575, MUID:94146218, PMID:7508758
 A:Accession: I46575
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-274 <ZHA>
 A:Cross-references: GB:I07786; NID:g164420; PIDN:AAAS3670.1; PID:g164421
 C:Superfamily: mouse mast cell growth factor

Query Match 84.8%; Score 899.5; DB 2; Length 274;
 Best Local Similarity 86.3%; Pred. No. 1,2e-64;
 Matches 176; Conservative 17; Mismatches 10; Indels 1; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLFFNPLVKTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWTLTCTIYQLLFFNPLVKTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60

QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
 Db 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120

QY 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPKDSRVSV 179
 Db 121 ENVKSSKSPPEPRLFTPEEPFRIFNRSIDAFKDFLEWVAPKTSVCVISTLTPEKDSRVSV 180

QY 180 TKFPMLPPVAASSLRNDSSSSNSK 203
 Db 181 TKFPMLPPVAASSLRNDSSSSNSK 204

RESULT 3

B61190
 mast cell growth factor, short form precursor - human
 M:Alternate names: kit ligand, short form; stem cell factor, short form
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
 C:Accession: B61190
 R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cammizzaro, L.
 Cell Growth Differ. 2, 373-378, 1991
 A:Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localize
 A:Reference number: A61190, MUID:92172791, PMID:1724381
 A:Accession: B61190
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-245 <AND>
 C:Comment: Alternative splicing produces this short form in which a predicted cleavage s
 C:Genetics:
 A:Gene: GDB:MGF
 A:Cross-references: GDB:128026; OMIM:184745
 A:Map position: 12q22-12q22
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: alternative splicing; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:187-209/Domain: transmembrane #status predicted <TMN>
 F:90,97,118,145/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 83.9%; Score 890; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 5.8e-64;
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFFNPLVKTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWTLTCTIYQLLFFNPLVKTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60

QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
 Db 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120

QY 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPK 173
 Db 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPK 173

RESULT 4

S47571
 stem cell factor, longer isoform - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S47571
 R:Zhou, J.H.; Hikono, H.; Onkaki, M.; Kubota, T.; Sakurai, M.
 Biochim. Biophys. Acta 1223, 148-150, 1994
 A:Title: Cloning and characterization of cDNAs encoding two normal isoforms of bovine st
 A:Reference number: S47571; MUID:94339176; PMID:7520283
 A:Accession: S47571
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-274 <ZHO>
 A:Cross-references: EMBL:D28934; NID:G538520; PIDN:BA06061.1; PID:G538521
 C:Superfamily: mouse mast cell growth factor

Query Match 83.6%; Score 886.5; DB 2; Length 274;
 Best Local Similarity 85.3%; Pred. No. 1.3e-63;
 Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLFFNPLVKTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWTLTCTIYQLLFFNPLVKTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60

QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
 Db 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120

QY 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPKDSRVSV 179
 Db 121 ENVKSSKSPPEPRLFTPEEPFRIFNRSIDAFKDFLEWVAPKTSVCVISTLTPEKDSRVSV 180

QY 180 TKFPMLPPVAASSLRNDSSSSNSK 203
 Db 181 TKFPMLPPVAASSLRNDSSSSNSK 204

RESULT 5

S58313
 stem cell factor precursor - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
 C:Accession: S58313
 R:McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
 submitted to the EMBL Data Library, August 1995
 A:Description: Molecular cloning and biological activity of ovine stem cell factor.
 A:Reference number: S58313
 A:Accession: S58313
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-202 <MC1>
 A:Cross-references: EMBL:Z50743; NID:G940807; PIDN:CAA90620.1; PID:G940808
 C:Superfamily: mouse mast cell growth factor

Query Match 83.5%; Score 885.5; DB 2; Length 202;
 Best Local Similarity 86.1%; Pred. No. 1e-63;
 Matches 174; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLFFNPLVKTEGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60

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Db      1 MKKQGTWITITITIIYQLLLFNPLVHTQGI CRRNRVVDVVDYTKLVANLPKQWMITLKYTPG 60
Qy      61 MDVLPSPHCWISIEWVAVQSLDLSITDLDKFSNISEGLSNYSIIDKLVNIIVDDIVECVENSS 120
Db      61 MDVLPSPHCWISIEWVQSLSVSLTDLDFKFSNISEGLSNYSIIDKLVKIVDDIVECMEBSHF 120
Qy      121 KDLKKSFPSPSPRLFTPEEPFRIFNRSTIDAKDF-VVASETSDCVWSTSLSPKDSRVSV 179
Db      121 ENVKSSSPSPPRQTPPEKFGIFPKSSIDAKFDLIVASTWSECVISTSPKDSRVSV 180
Qy      180 TKPFMLPPVAASSLRNDSSSSN 201
Db      181 TKPFMLPPVAASSLRNDSSSSN 202

RESULT 6
146929
stem cell factor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jul-2000
C:Accession: I46929
R:Shull, R.M.; Suggs, S.V.; Langley, K.E.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
Exp. Hematol. 20, 1118-1124, 1992
A:Title: Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic F
A:Reference number: I46929; MUID:93106145; PMID:1281786
A:Accession: I46929
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-274 <SHU>
A:Cross-references: GB:SS3329; NID:g262240; PIDN:AMB24619.1; PID:g262241
C:Superfamily: mouse mast cell growth factor

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Query Match      81.3%; Score 862.5; DB 2; Length 274;
Best Local Similarity 84.8%; Pred. No. 1,1e-61;
Matches 173; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

QY      1 MKKTQWTWLTTCIYQLQLFNPVLVKTGECIRNRVTNNVADVTKLVANLPKDYMTLTKVVP 60
DB      1 MKKTQWTWLTTCIYQLQLFNPVLVKTGECGRKRVTDVQKDYTKLVANLPKDYMTLTKVVP 60
QY      61 MDVLPSCWISERNVQVQSDSLTDLIDKFSNISSEGLSNYSITDKLVNIYDDLVECKENSS 120
DB      61 MDVLPSCWISVWVEQSLVSLTDLIDKFSNISSEGLSNYSITDKLVNIYDDLVECKEYSF 120
QY      121 KDLKKSFSFSPERPLTPEEFRIINRSIDAKDP-VVASEISDCVSSSTISPEKDSVSV 179
DB      121 ENVKKAPSPSELRFTPEEFRIINRSIDAKDETVASKSECVSSSTISPEKDSRVSV 180
QY      180 TKPEMLPPVAASSLRNDSSSNSK 203
DB      181 TKPEMLPPVAASSLRNDSSSNSRK 204

RESULT 7
B35974
Stem cell factor protein precursor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: B35974; A39605
R:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
B:J.C.; Patel, A.C.; Fisher, E.F.; Ejlavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, R.
A:Title: Primary structure and functional expression of rat and human stem cell factor D
A:Reference number: A35974; MUID:91004219; PMID:2208279
A:Accession: B35974
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-201 <MAR>
A:Cross-references: GB:M59966; NID:9206861; PIDN:AAA42117.1; PID:9554507
R:Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiata, E.A.; Zeebo,
J. Biol. Chem. 266, 8102-8107, 1991
A:Title: Amino acid sequence and post-translational modification of stem cell factor iso

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[illegible]

RESULT 8
565801
mast cell growth factor - mouse
N:Alternate names: hematopoietic growth factor KL, ligand steel factor; stem cell factor
C:Species: Mus musculus (house mouse)
C:date: 28-Oct-1996 #sequence revision 27-Feb-1997 #text change 01-Dec-2000
C:Accession: S65801; A43751; A35977; A35972; A35975; A35973; I48768
R:Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
Genetics 142, 927-934, 1996
A:Title: Multiple pathways for Steel regulation suggested by genomic and sequence analysis
A:Reference number: S65801; MUID:97002531; PMID:884898
A:Accession: 565801
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-273 <BED>
A:Cross-references: EMBL:U44725; NID:g1172215; PID:AAC52447.1; PID:g1172216
R:Huang, B.U.; Nocka, K.H.; Buck, J.; Besmer, P.
Mol. Biol. Cell 3, 349-362, 1992
A:Title: Differential expression and processing of two cell associated forms of the kit-
A:Reference number: A43751; MUID:92330001; PMID:1378337
A:Accession: A43751
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-214, V, 216-273 <HUA>
A:Cross-references: GB:S540364; NID:g251668; PID:AAB22554.2; PID:g5705957
A>Note: the authors translated the codon TTG for residue 215 as Trp
R:Huang, B.; Nocka, K.; Beter, D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Leder
Cell 63, 225-233, 1990
A:Title: The hematopoietic growth factor KL is encoded by the Sl locus and is the ligand
A:Reference number: A35976; MUID:91004221; PMID:1698557
A:Accession: A35976
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206, S', 208-270 <HU2>
A:Cross-references: GB:M38511
R:Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; March,
Cell 63, 235-243, 1990
A:Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active in
A:Reference number: A35977; MUID:91004223; PMID:1698558
A:Accession: A35977
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-273 <AND>
A:Cross-references: GB:M57647; GB:M38436; NID:g199151; PID:AAA39538.1; PID:g199152
R:Copeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.J.; Jenkins, N.A.; Cosman, D.; An

Cell 63, 175-183, 1990
A:Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and is
A:Reference number: A35972; MUID:91004216; PMID:169854
A:Accession: A35972
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 26-53 <COP>
A:Cross-references: GB:M5912
R:Zebo, K.M.; Williams, D.A.; Geisler, E.N.; Broudy, V.C.; Martin, F.H.; Atkins, H.L.;
Cattanch, B.M.; Galli, S.J.; Suggs, S.V.
Cell 63, 213-224, 1990
A:Title: Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for
A:Reference number: A35975; MUID:91004220; PMID:169856
A:Accession: A35975
A:Molecule type: mRNA
A:Residues: 1-201 <ZSE>
A:Cross-references: GB:M5915; NID:9200935; PIDN:AAA40095.1; PID:G554271
R:Zebo, K.M.; Wypych, J.; McNiece, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev,
A.: Langley, K.E.
Cell 63, 195-201, 1990
A:Title: Identification, purification, and biological characterization of hematopoietic
A:Reference number: A35973; MUID:91004218; PMID:2208278
A:Accession: A35973
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 27-29, 'R', '31-39 <ZS2>
R:Brannan, C.I.; Bedell, M.A.; Resnick, J.L.; Eppig, J.J.; Handel, M.A.; Williams, D.E.;
Genes Dev. 6, 1832-1842, 1992
A:Title: Developmental abnormalities in Steel17H mice result from a splicing defect in t
A:Reference number: A44071; MUID:93012940; PMID:1383087
A:Accession: 148768
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206, 'S', 208-273 <RBS>
A:Cross-references: EMBL:X68989; NID:9395283; PIDN:CAA48778.1; PID:9395284
C:Genetics:
A:Gene: Slf
A:Map position: 10
C:Superfamily: mouse mast cell growth factor
C:Keywords: extracellular protein; glycoprotein; transmembrane protein

Query March 80.6%; Score 855; DB 2; Length 273;
Best Local Similarity 82.3%; Pred. No. 4, 2e-61;
Matches 167; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWTWITTCYIQLLFLNPLVKTEGICRNKRVNNVQDVKLVANLPEKDYMITLKXVPG 60
DB 1 MKKTQWTWITTCYIQLLFLNPLVKTEGICGNPYVDNVQDITKLVANLPEKDYMITLVNAG 60
QY 61 MDVLPSCWISBEMVQVLSLTDLLDKFSNISSEGISNYSIIDKLVINIVDDIVECKENSS 120
DB 61 MDVLPSCWMLDVMQVLSLSTLTLLDKFSNISSEGISNYSIIDKLGKIVDDVLVMEENAP 120
QY 121 KDILKSPSPSPRLTTPPEFRIFNRSIDAFKDFVVAESITSDCVSSSTLSPEKDSRVSYT 180
DB 121 KNIKSPSPRPRTSTPEEPFSIFNRSIDAFKDFVVAESITSDCVLSSTLGPKEKDSRVSYT 180
QY 181 KPFMLPVAASLRDSSSSNSK 203
DB 181 KPFMLPVAASLRDSSSSNSRK 203

RESULT 9
A37934
N:Alternate names: KL-2 protein
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000
C:Accession: A37934; B43751
R:Flanagan, J.G.; Chan, D.C.; Leder, P.
Cell 64, 1025-1035, 1991
A:Title: Transmembrane form of the kit ligand growth factor is determined by alternative
A:Reference number: A37934; MUID:91160046; PMID:1705866

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A:Accession: A37934
A:Molecule type: mRNA
A:Residues: 1-245 <FLA>
A:Cross-references: GB:M64262
R.Huang, E.J.; Nocka, K.H.; Buck, J.; Beemer, P.
Mol. Biol. Cell 3, 349-362, 1992
A>Title: Differential expression and processing of two cell associated forms of the kit-
A:Reference number: A43751; MUID:92330001; PMID:1378327
A:Accession: B43751
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-173, 'R', '175-186, 'L', '188-245 <HUA>
A:Cross-references: GB:S04534
A>Note: The authors translated the codon TTG for residue 187 as Tyr
C:Superfamily: mouse mast cell growth factor

Query Match      67.4%; Score 715; DB 2; Length 245;
Best Local Similarity 79.8%; Pred. No. 5.8e-50;
Matches 138; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY      1 MKKTQWILTCIVTQLLEFNLVKTSGICNRRVTNNVKDXTKLVANLPKDYMILLTKVPV 60
        |||:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       1 MKKTQWITITCIQLLENPLVKTKEICGNPVDNKDTKVLVANLENDYMITLLNVAG 60
        |||:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY      61 MDVLPSCWISSEMWVQLSDSLTDLDKFNSISGLSNYSIIDKLVIIVDDLVECVENSS 120
        |||:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       61 MDVLPSCWLRDMVITQLSLTLTLDKFSNISGLSNYSIIDLKGKIVDDLVLCMEBNAP 120
        |||:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY      121 KDCLKSKSKSEPRRLFTPEEFRIFNRSIDFKCPVVAASEISDCVSSSTLSPEK 173
        :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB       121 KNIKESKRREPTSGFPPEEFPFSIFNRSIDAFKDFMAASDTSDCVLSSTLGPEK 173
        :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 10
S29052
stem cell factor - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: S29052
R:Lu, H.S.; Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderek, K.; Baltera J.; Langley, K.E.
Arch. Biochem. Biophys. 298, 150-158, 1992
A:Title: Post-translational processing of membrane-associated recombinant human stem cell
A:Reference number: S29052; MUID:92398336; PMID:1381905
A:Accession: S29052
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-113;4-10;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
C:Superfamily: mouse mast cell growth factor

Query Match      54.3%; Score 576.5; DB 2; Length 124;
Best Local Similarity 75.2%; Pred. No. 2,9e-39;
Matches 124; Conservative 0; Mismatches 0; Indels 41; Gaps 4;

Cy 26 EGIQRNVTVNNVDVTKLVANLPKDMITLKYYPGMDVYPSHCWISENVVQSDSLTDLL 85
    |||||
Db 1 EGICRNVTNNVK-----DVLPSCWISENVVQLS----- 30

Cy 86 DKFNSISEGSLNYSIIDKLVINIVDDIVECYKENSKDCLKSFKSPPEPLFTPEEPRIFN 145
    |||||
Db 31 DKFNSISEGSLNYSII-----DDIVECYKENSKDCLKSFKSPPEPLFTPEEPRIFRN 83

Cy 146 RSIDAFKDFVAVSETSDCVVSTLSPEKDSRVSVTRKPFMLPVAA 190
    |||||
Db 84 RSI----DFVAVSETSDCVVSTLSPEKDSRVSVTRKPFMLPVAA 124

RESULT 11
S70366
stem cell factor long form precursor - guai1
C:Species: Coturnix coturnix (quail)
C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C:Accession: S70366

```

R.Petit, J.N., Kulik, M.J. Biochim. Biophys. Acta 1307, 149-151, 1996
 A>Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell factor
 A:Reference number: S70366; PMID:8679698

Query Match	53.8%	Score	570.5	DB 2	Length	287			
Best Local Similarity	55.1%	Pred. No.	2.6e-38						
Matches	114	Conservative	37	Mismatches	51	Indels	5	Gaps	3

```

QY      61 MDVLPSCWISAMVQVSDSLTDLIDKF--SNISEGLSNYSIIDKLVINVDVLVCVXE 117
Db      61 MDSLPNCWHLHMLVPEFSRSLNHLQKPFVIDSDMSDVLSNYSIIINLTRLINDLMACLAF 120

QY      118 NSSKO-LKKSFSPEPRLLTPPEEFFIIFNRSIDAFDPVVAASGTSPQVASSITL-SPKKS 175
Db      121 DKNKDFIKENGHLYEEDRFIIPENFPFLFRRTIEVVEYKFPADSLDKDCIMPSIVETEPDSS 180

QY      176 RVSATKPFMLPVAASSLRNDSSSSSS 202
Db      181 RVAAVTKTISFPVAASSLRNDISGSNT 207

```

RESULT 12
JN0637
stem cell factor precursor (chicken)
C:Species: Gallus gallus (chicken)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #next_change 21-Jul-2000
C:Accession: JN0637
R:Zhou, J.H.; Ohtaki, M.; Sakurai, M.
Gene 127, 269-270, 1993
A:Title: Sequence of a cDNA encoding chicken stem cell factor.
A:Reference number: JN0637; MUID:93273244; PMID:7684722
A:Accession: JN0637
A:Molecule type: mRNA
A:Residues: 1-287 <ZHO>
A:Cross-references: GB:DJ3516; NID:g391648; PIDD:BAA02733.1; PID:g391649
A:Experimental source: brain
C:Superfamily: mouse mast cell growth factor
C:Keywords: growth factor; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <Sig>
F:126-287/Product: stem cell factor #status predicted <MAT>
F:126-248/Domain: transmembrane #status predicted <TM>

	Query Match	53.0%	Score 563.5:	DB 2:	Length 287;
	Best Local Similarity	54.6%*	Pred. No. 1.1e-37;		
	Matches 113;	Conservative 36;	Mismatches 53;	Indels 5;	Gaps 3
QY	1	MKKTQTWLTTCYTLLLEFNPLVKEGICRRNRVTNNVKKVTKLVANLPRDYMTTLKYVPG	60		
		: : : : : : : : : : : : : : : : :			
Db	1	MKAQGTWITTCCTCLQLLLNLPVKQGSSCGNPPTDDVDNIATKVGLPNDYLITLKAYPK	60		
		: : : : : : : : : : : : : : : : :			
QY	61	MDVLPSHCITISEMVAQLSDSLTDLDKESNT---SEGLSNYSIIDKLVINIVDDLYECKVE	117		
		: : : : : : : : : : : : : : : : :			
Db	61	MSLPLPHCWLHMLMVPEFSRSLHNLLQKFSDISDMSDVLSNYSINILRTIRINDIMWACIAF	120		
		: : : : : : : : : : : : : : : : :			
QY	118	NSSGD-LIKSPKSPEERLFTPEEFPRIPKRSIDAQDFVASSTDPQVVSSTL-SPEKAS	175		
		: : : : : : : : : : : : : : : : : : :			
Db	121	DNKQPIKNGHLYEEDRFIPEAFFFLFNFSTIEVYEKFADSLKDNCDCIMPSTIVEITENDS	180		
		: : : : : : : : : : : : : : : : : : :			
QY	176	RVSVTKPFLPVAASSLANDSSSNS	202		

Db 181 RVAVTKTISFPVVAASSLRNDISGNT 207

RESULT 13
 S70367
 stem cell factor short form precursor - quail
 C:Species: Coturnix coturnix (quail)
 C:Date: 06-Dec-1996 #sequence #revision 25-Apr-1997 #text_change 21-Jul-2000
 C:Accession: S70367
 R:Petitje, J.N.; Kulik, M.J.
 Biochim. Biophys. Acta 1307, 149-151, 1996
 A>Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell fac
 #:Reference number: S70366; MUID:96283808; PMID:8679658

Query Match	45.2%	Score 479.5	DB 2	Length 253
Best Local Similarly	46.9%	Pred. No. 4.1e-31		
Matches 100; Conservative	42;	Mismatches 58;	Indels 13;	Gaps 4

```

Qy      MKKTOWMILITCJYLQLLMLFNPLVPTKEGICRRRATNNVADVTKJVAAN.PXQYMTLTKKVP 60
Db      1 MKKAQWMIITTCCLQQLLNLPLVKTQSCGCPVDDVNDLAKLVGNLPNDYLLTLTKKVP 60

Qy      61 MDVLPSCWISSEWVQVQSDSLTDLIDKE---SNISEG.SVNSYIIDKLVNIVDDLVECVKE 117
Db      61 MDSLPWHCHLHWVEFSSKSLNLLQKRVDSIDMSDVLSVNSIINNLTIRIINDLMACIAP 120

Qy      118 NSSKD-LKKSFKSPPEPRLFTPEEPFRIRNRSIDAFKQDFVASETSDCVASSTL-SPEKDS 175
Db      121 DKNKDFIKENGHLYEEDRFPIPENFRLTFRNRTIEVKEFADSLDKNDICIMPSTVETPENEE 180

Qy      176 RVSVTKEPMLPRVYASSLRNDSSSNKXYILI 208
Db      181 ALGF-----ISSSLQGISIALTSLSLILI 205

```

RESULT 14
B35971
mast cell growth factor - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C/Accession: B35971
R/Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.
Cell 63, 167-174, 1990
A/Title: Identification of a ligand for the c-kit proto-oncogene.
I/Reference number: A35971; MUID:91004215; PMID:168553

Query Match	16.5%	Score 175.5	DB 2	Length 51
Best Local Similarity	72.3%	Pred. No. 1.1e-07		
Matches 34; Conservative	5; Mismatches 7			Indels 1; Gaps 1

```

QY      28  ICRNNVTNNVXDVTGLVANI.PCDNMITLKCVCVGMIDL.PSHCWTSEMV  74
          | | | | | | | | | | | | | | | | | | | | | | | |
Db      3  ICGNEVDVWAKDITGLVANI.PNDVITLTVYAGMDVLPF--WVDDNVI  48

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:42:38 / Search time 6.58953 Seconds

(without alignments)
1484.408 Million cell updates/sec

Title: US-09-224-683-46

Perfect score: 1061

Sequence: 1 MKKTQTWLTCTIYQLLFFN.....AASSLRNDSSSSSKYIYL 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1030	97.1	273	1 SCF_HUMAN	P21583 homo sapien
2	908.5	85.6	274	1 SCF_FELCA	P79169 felis silve
3	899.5	84.8	274	1 SCF_PIG	Q29030 sus scrofa
4	898.5	84.7	274	1 SCF_HORSE	Q95nd2 equus caball
5	889.5	83.8	267	1 SCF_SHEEP	P79368 ovis aries
6	886.5	83.6	274	1 SCF_BOVIN	Q28132 bos taurus
7	885.5	83.5	274	1 SCF_CAPI	Q95m19 capra hircu
8	862.5	81.3	274	1 SCF_CANFA	Q06220 canis famli
9	861	81.1	273	1 SCF_RAT	P21581 rattus norv
10	859.5	81.0	274	1 SCF_MUSVI	Q95n18 mus muscla
11	855	80.6	273	1 SCF_MOUSE	P20826 mus musculu
12	570.5	53.8	287	1 SCF_COTJA	Q90314 coturnix co
13	562.5	53.0	287	1 SCF_CHICK	Q09108 gallus gall
14	102	9.6	981	1 SCFA_RICFE	Q9a337 rickettsia
15	94	8.9	1813	1 UN13_CABEL	P27175 caenorhabdi
16	92	8.7	935	1 COG_YEAST	P32074 saccharomyc
17	91.5	8.6	496	1 MURE_WIGBR	Q8d221 wigleswort
18	90.5	8.5	1742	1 MYSC_HUMAN	Q9nq24 homo sapien
19	89	8.4	989	1 PTP3_DICDI	P54637 dicystosella
20	88.5	8.3	545	1 VNC5_JCDNV	Q90054 junonia coe
21	87.5	8.2	966	1 CAPP_MEDSA	Q02735 medicago sa
22	87	8.2	664	1 2AAB_CABEL	Q09543 caenorhabdi
23	86.5	8.2	844	1 BRO1_YEAST	P48582 saccharomyc
24	85.5	8.1	623	1 SYR_SUITO	Q971X1 sulfolobus
25	84.5	8.0	466	1 DNAA_PROMI	P22817 proteus mir
26	84.5	8.0	964	1 CAPP_TOBAC	P27154 nicotiana t
27	84.5	8.0	998	1 SCAD_RICAK	Q9a1X9 rickettsia
28	83	7.8	875	1 UBAP_SCHPO	Q9p755 schizosacia
29	82.5	7.8	451	1 DNAA_PASMU	Q9c1d4 pasteurella
30	82.5	7.8	991	1 SCAD_RICAU	Q9a164 rickettsia
31	82	7.7	235	1 PYRH_UREPA	Q9p466 ureaplasma
32	82	7.7	1140	1 YM96_YEAST	Q04893 saccharomyc
33	82	7.7	1188	1 PPSA_METUA	Q57962 methanococc

34	82	7.7	1224	1 MSNS_YEAST	P52918 saccharomyc
35	81	7.6	196	1 KITH_ASFB7	P18555 african swi
36	81	7.6	388	1 YA25_METUA	Q58431 methanococc
37	81	7.6	490	1 CPCK_MACRA	P33262 macaca fasc
38	81	7.6	626	1 GIDA_BUCBP	P59485 buchnera ap
39	80.5	7.6	373	1 BIOF_HELPJ	Q921N1 helicobacte
40	80.5	7.6	442	1 YBHI_ECOLI	P32690 escherichia
41	80.5	7.6	755	1 P100_HSVJ7	P52519 human herpe
42	80.5	7.6	1039	1 PDP2_ARATH	Q9m9w8 arabidopsis
43	80.5	7.6	2238	1 RPL2_BUNYW	P20470 bunyamwera
44	80.5	7.6	4563	1 APB_HUMAN	P04114 homo sapien
45	80	7.5	480	1 YB9Q_YEAST	P38348 saccharomyc

ALIGNMENTS

RESULT 1	ID	SCF_HUMAN	STANDARD:	PRT:	273 AA.
AC	P21583	Q16487: Q9UOK7:			
DT	01-MAY-1991	(Rel. 18, Created)			
DT	01-MAY-1991	(Rel. 18, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).				
GN	KITLG OR MGF OR SCF				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=91004219; PubMed=2208279;				
RA	Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,				
RA	Morris C.F., McNeice I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,				
RA	Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,				
RA	Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,				
RA	Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zeebo K.M.,				
RT	"Primary structure and functional expression of rat and human stem				
RT	cell factor DNAs."				
RL	Cell 63:203-211(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RX	MEDLINE=99160429; PubMed=10049787;				
RA	Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.,				
RT	"Parathyroid hormone-regulated production of stem cell factor in human				
RT	osteoblasts and osteoblast-like cells."				
RL	Biochem. Biophys. Res. Commun. 255:778-784(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Han C., Peng X., Yuan J., Qiang B.;				
RT	Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE OF 167-248 FROM N.A. (ISOFORM 2).				
RX	MEDLINE=92360843; PubMed=1379846;				
RA	Toyota M., Hinoda Y., Itoh F., Tsujisaki M., Imai K., Yachi A.;				
RT	"Expression of two types of Kit ligand mRNAs in human tumor cells."				
RL	Int. J. Hematol. 55:301-304(1992).				
CC	-1- FUNCTION: Stimulates the proliferation of mast cells. Able to				
CC	augment the proliferation of both myeloid and lymphoid				
CC	hematopoietic progenitors in bone marrow culture. Mediates also				
CC	cell-cell adhesion. Acts synergistically with other cytokines,				
CC	probably interleukins.				
CC	-1- SUBUNIT: Homodimer, non-covalently linked (Probable).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).				
CC	Also exists as a secreted soluble form (isoform 1 only) (By				
CC	similarity).				
CC	-1- ALTERNATIVE PRODUCTS:				
CC	Event=Alternative splicing; Named isoforms=2;				
CC	Name=1; Synonyms=SCF248;				
CC	Isoid=P21583-1; Sequence=Displayed;				
CC	Name=2; Synonyms=SCF220;				


```

QY 1 MKKTQWITTCIYLLQLLFNPLVTEGICRNVTNNVKQVTKLVANLPKQWITTKYVPG 60
DB 1 MKKTQWITTCIYLLQLLFNPLVTEGICRNVTNNVKQVTKLVANLPKQWITTKYVPG 60
QY 61 MDVLPSCWISSEWVQSLVSLTDLKPSNISSEGLSNYSIIDLVNIYVDLVCEVCKENSS 120
DB 61 MDVLPSCWISSEWVQSLVSLTDLKPSNISSEGLSNYSIIDLVNIYVDLVCEVCKENSS 120
QY 121 KDLKSKFSKSPERLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKDSRVSV 179
DB 121 ENVKSSKSPERLFTPEEFRIFNRSIDAFKDFLEWVAKTSECVCVISTLSPKDSRVSV 180
QY 180 TKPFMLPVAASSLRNDSSSSNSK 203
DB 181 TKPFMLPVAASSLRNDSSSSNSK 204

RESULT 3
SCF_PIG STANDARD; PRT; 274 AA.
AC 029030;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast
  cell growth factor) (MGF).
GN KITLG OR MGF.
OS Sus acrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
ON NCBI_TaxID=9823;
RX SEQUENCE FROM N.A.
RC TISSUE=Uterus;
  MEDLINE=94146218; PubMed=7508758;
  Zhang Z., Anthony R.V.;
  "Poringe stem cell factor/c-kit ligand: its molecular cloning and
  localization within the uterus.";
  Biol. Reprod. 50:95-102(1994).
RL
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
  augment the proliferation of both myeloid and lymphoid
  hematopoietic progenitors in bone marrow culture. Mediates also
  cell-cell adhesion. Acts synergistically with other cytokines,
  probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
  secreted soluble form (By similarity).
CC -1- PTM: A soluble form is produced by proteolytic processing of
  the extracellular domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L07786; AAA53670.1; -.
DR PIR; I46575; I46575.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF.1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT CHAIN 1 25
FT SIGNAL 1 25
FT CHAIN 26 274
FT SIGNAL 26 274
FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 POTENTIAL.
FT DOMAIN 239 274 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 114 BY SIMILARITY.
FT CARBOHYD 68 164 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 274 AA; 3118 MW; FF3C871AD7BA6A6 CRC64;
Query Match
Best Local Similarity 84.8%; Score 899.5; DB 1; Length 274;
Matches 176; Conservative 17; Mismatches 10; Indels 1; Gaps 1;
QY 1 MKKTQWITTCIYLLQLLFNPLVTEGICRNVTNNVKQVTKLVANLPKQWITTKYVPG 60
DB 1 MKKTQWITTCIYLLQLLFNPLVTEGICRNVTNNVKQVTKLVANLPKQWITTKYVPG 60
QY 61 MDVLPSCWISSEWVQSLVSLTDLKPSNISSEGLSNYSIIDLVNIYVDLVCEVCKENSS 120
DB 61 MDVLPSCWISSEWVQSLVSLTDLKPSNISSEGLSNYSIIDLVNIYVDLVCEVCKENSS 120
QY 121 KDLKSKFSKSPERLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKDSRVSV 179
DB 121 ENVKSSKSPERLFTPEEFRIFNRSIDAFKDFLEWVAKTSECVCVISTLSPKDSRVSV 180
QY 180 TKPFMLPVAASSLRNDSSSSNSK 203
DB 181 TKPFMLPVAASSLRNDSSSSNSK 204

RESULT 4
SCF_HORSE STANDARD; PRT; 274 AA.
AC 095MD2; 062765; 095MG7; 095MG8; 09W1Y5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast
  cell growth factor) (MGF).
GN KITLG OR MGF OR SCF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
ON NCBI_TaxID=9796;
RX SEQUENCE OF 4-264 FROM N.A.
RC TISSUE=Skin;
  Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
  "An Equine sequence homologous to stem cell factor (KIT-ligand).";
  Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RL
RN [1]
RN SEQUENCE OF 107-202 AND 227-274 FROM N.A.
RN Terry R.R., Bailey E.F., Cochran E.G.;
  "Evaluation of MGF as the candidate gene for Appaloosa spotting.";
  Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE OF 147-197 FROM N.A.
RN Caetano A.R., Shine Y.-L., Lyons L.A., Laughlin T.F., O'Brien S.J.,
  Murray J.D., Bowling A.T.;
  "A primary Human-Horse comparative gene map.";
  Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
  augment the proliferation of both myeloid and lymphoid
  hematopoietic progenitors in bone marrow culture. Mediates also
  cell-cell adhesion. Acts synergistically with other cytokines,
  probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
  secreted soluble form (By similarity).
CC -1- PTM: A soluble form is produced by proteolytic processing of
  the extracellular domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----

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DR	EMBL; AF401625;	AAK94474.1;	-
DR	EMBL; AF05198;	AAC97076.1;	-
DR	EMBL; AF367704;	AAK63249.1;	-
DR	EMBL; AF367706;	AAK63250.1;	-
DR	EMBL; AF130770;	AAK6716.1;	-
DR	InterPro: IPR003452;	SCF.	-
DR	Pfam: PF02404;	SCF; 1.	-
KM	Growth factor;	Glycoprotein;	Transmembrane; Signal; Cell adhesion
FT	SIGNAL	1	POTENTIAL.
FT	CHAIN	26	274
FT	DOMAIN	26	215
FT	TRANSMEM	216	238
FT	DOMAIN	239	274
FT	DISULFID	29	114
FT	DISULFID	68	164
FT	CARBOHYD	90	90
FT	CARBOHYD	97	97
FT	CARBOHYD	145	145
FT	CARBOHYD	196	196
FT	CARBOHYD	207	207
FT	CONFLICT	15	15
FT	CONFLICT	241	241
Q	SEQUENCE	274 AA;	31217 MW; 96CID4C905913JF2 CRC64;

"Ovine stem cell factor gene is located within a syntenic group on chromosome 3 conserved across mammalian species";
Mamm. Genome 7:472-473 (1996).
[2]
SEQUENCE OF 1-202 FROM N.A.
McInnes C.J., Logan M., Falcione V.M., Rawlins P., Huntly J., Haig D.,
factor.
Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
-i- FUNCTION: Stimulates the proliferation of mast cells. Able to
augment the proliferation of both myeloid and lymphoid
hematopoietic progenitors in bone marrow culture. Mediates also
cell-cell adhesion. Acts synergistically with other cytokines,
probably interleukins (By similarity).
-i- SUBUNIT: Homodimer, non-covalently linked (Probable).
-i- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
secreted soluble form (By similarity).
-i- PTM: A soluble form is produced by proteolytic processing of
the extracellular domain (By similarity).
-i- SIMILARITY: BELONGS TO THE SCF FAMILY.

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or send an email to license@isb-sib.ch).

DR	EMBL; U89874; AAB49491.1; -		
DR	EMBL; Z50743; CAA90620.1; -		
DR	PIR; S58313; S58313.		
DR	InterPro; IPR003452; SCF.		
DR	Pfam; PF02404; SCF.1.		
KM	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.		
FT	SIGNAL	1	25
FT	CHAIN	26	>267
FT	DOMAIN	26	215
FT	TRANSMEM	216	238
FT	DOMAIN	239	>267
FT	DISULFID	29	114
FT	DISULFID	68	164
FT	CARBOHYD	90	90
FT	CARBOHYD	97	97
FT	CARBOHYD	145	145
FT	CARBOHYD	196	196
FT	NON TER	267	267
EQ	SEQUENCE	267 AA;	30148 MW; 9D9D959E4B9EC841 CRC64;

AC Q28132; Q9TU74;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Maat
 cell growth factor) (MGF).
 GN KITLG OR SCF.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Spleen;
 RX MEDLINE=94339176; PubMed=7520283;
 RA Zhou J., Hikono H., Ohtaki M., Kubota T., Sakurai M.;
 RT "Cloning and characterization of cDNAs encoding two normal isoforms of
 RT bovine stem cell factor."
 RL Biochim. Biophys. Acta 1223:148-150(1994).
 RL [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal brain;
 RA Kudo T.;
 RT "Bovine counterpart of stem cell factor."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE OF 204-239 FROM N.A., AND VARIANT ASP-218.
 RC STRAIN=Belgian Blue;
 RX MEDLINE=99315331; PubMed=10384045;
 RA Seitz J.J., Schmutz S.M., Thue T.D., Buchanan F.C.;
 RT "A missense mutation in the bovine MGF gene is associated with the
 RT roan phenotype in Belgian Blue and Shorthorn cattle."
 RL Mamm. Genome 10:710-712(1999).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins (By similarity).
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
 CC Also exists as a secreted soluble form (isoform 1 only) (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q28132-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q28132-2; Sequence=VSP 006020;
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC isoform 1 in the extracellular domain (By similarity).
 CC -1- POLYMORPHISM: The roan locus is responsible for the coat
 CC coloration of Belgian Blue and Shorthorn cattle. The solid-colored
 CC and white animals are homozygotes, and the roan animals, with
 CC intermingled colored and white hairs, are heterozygous. The roan
 CC phenotype is due to the Asp-218 mutation.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D28934; BA06061.1; -
 DR EMBL: AB033716; BA94808.1; -
 DR EMBL: AF120154; AA05535.1; -
 DR PIR: S47571; S47571.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF. 1.
 KM Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;

KM Alternative splicing; Polymorphism.
 FT SIGNAL 1 25
 FT CHAIN 26 274
 FT DOMAIN 26 215
 FT TRANSMEM 216 238
 FT DOMAIN 239 274
 FT DISULFID 29 114
 FT DISULFID 68 164
 FT CARBOHYD 90 90
 FT CARBOHYD 145 145
 FT CARBOHYD 196 196
 FT VARSPLIC 175 203
 FT FT
 FT FT
 SQ VARIANT 218 218 /FTID=VSP 006020.
 SQ SEQUENCE 274 AA, 31014 MW, 64128 CRC64;
 Query Match 83.6%; Score 886.5; DB 1; Length 274;
 Best Local Similarity 85.3%; Pred. No. 1.1e-61;
 Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;
 QY 1 MKKTQWILTCYLLQLLFNPLVKTGICRNRYTNVADYTLVANLPDQWITTKYVPG 60
 DB 1 MKKTQWILTCYLLQLLFNPLVKTGICRNRYTNVADYTLVANLPDQWITTKYVPG 60
 QY 61 MDVLPBHCWISPMVQLDSLTDLLDKPSNISSEGLSNYSIIDKLVNVDVLYECVKENS 120
 DB 61 MDVLPBHCWISPMVQLDSLTDLLDKPSNISSEGLSNYSIIDKLVNVDVLYECVKENS 120
 QY 121 KDLKSKFSPSPRLFTPEEFRIFNRSIDAFDPF-VVASETSDCVVSSTLSPKSRVSV 179
 DB 121 EHVKKSSKSPSPRLFTPEEFRIFNRSIDAFDPF-VVASETSDCVVSSTLSPKSRVSV 180
 QY 180 TRPMLPVAASGLRNDSSSSNSK 203
 DB 181 TRPMLPVAASGLRNDSSSSNSK 204
 RESULT 7
 SCF_CAPHI STANDARD; PRT; 274 AA.
 ID SCF_CAPHI
 AC Q95MI9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Maat
 cell growth factor) (MGF).
 GN KITLG OR SCF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Shiba; TISSUE=Brain;
 RA Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;
 RT "Identification of splicing isoforms of caprine stem cell factor
 RT (gSCF) transcripts and expression patterns of the two major isoforms,
 RT gSCF325 and gSCF741, in the brain and the skin of adult and fetal
 RT Shiba goats, Capra hircus."
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins (By similarity).
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
 CC secreted soluble form (By similarity).
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC the extracellular domain (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.

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CC EMBL: AB002152; BAB71753.1; -
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF. 1.
 KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 FT CHAIN 1 25
 FT DOMAIN 26 215
 FT TRANSMEM 216 238
 FT DOMAIN 239 274
 FT DISULFID 29 114
 FT DISULFID 68 164
 FT CARBOHYD 90 90
 FT CARBOHYD 97 97
 FT CARBOHYD 145 145
 FT CARBOHYD 196 196
 SQ SEQUENCE 274 AA; 31052 MW; BPF669A509EF65D CRC64;

Query Match 83.5%; Score 885.5; DB 1; Length 274;
 Best Local Similarity 85.3%; Pred. No. 1.3e-61;
 Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYVPG 60
 DB 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYVPG 60

QY 61 MDVLPBHCWISENVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
 DB 61 MDVLPBHCWISENVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120

QY 121 KDLKSFKSPPRPFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPKDSRVSV 179
 DB 121 ENVKKSPSPPRPFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPKDSRVSV 180

QY 180 TKPFMLPVAASLRNDSSSSNSK 203
 DB 181 TKPFMLPVAASLRNDSSSSNSK 204

RESULT 8
 SCF CANFA STANDARD; PRT; 274 AA.
 AC 006220; O8SPM6;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cell growth precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
 DE cell growth factor) (MGF).
 GN KITLG OR MGF.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN (1) SEQUENCE FROM N.A.
 RP TISSUE=T-cell;
 RC MEDLINE=93106145; PubMed=1281786;
 RX SHULL R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W.,
 RA "Canine stem cell factor (C-kit ligand) supports the survival of
 RT hematopoietic progenitors in long-term canine marrow culture.";
 RN Exp. Hematol. 20:1118-1124 (1992).
 RN (2) SEQUENCE OF 17-274 FROM N.A.
 RC TISSUE=tail;

RA Schmutz S.M., Berrere T.G.;
 RT "MGF sequencing in the dog aids in mapping to CFA15";
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBP databases.
 CC -!- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins.
 CC -!- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -!- SECRETED SOLUBLE FORM.
 CC -!- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -!- PTM: A soluble form is produced by proteolytic processing of
 CC the extracellular domain (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SCF FAMILY.

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CC EMBL: S53329; AAB24619.1; -
 DR EMBL: AY094361; AAM16280.1; -
 DR PIR: I46929; I46929.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF. 1.
 KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 FT CHAIN 1 25
 FT DOMAIN 26 215
 FT TRANSMEM 216 238
 FT DOMAIN 239 274
 FT DISULFID 29 114
 FT DISULFID 68 164
 FT CARBOHYD 90 90
 FT CARBOHYD 97 97
 FT CARBOHYD 145 145
 FT CARBOHYD 196 196
 SQ SEQUENCE 274 AA; 30869 MW; 4182B9AD00793B CRC64;

Query Match 81.3%; Score 862.5; DB 1; Length 274;
 Best Local Similarity 84.8%; Pred. No. 7.8e-60;
 Matches 173; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYVPG 60
 DB 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYVPG 60

QY 61 MDVLPBHCWISENVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
 DB 61 MDVLPBHCWISENVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120

QY 121 KDLKSFKSPPRPFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPKDSRVSV 179
 DB 121 ENVKKSPSPPRPFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPKDSRVSV 180

QY 180 TKPFMLPVAASLRNDSSSSNSK 203
 DB 181 TKPFMLPVAASLRNDSSSSNSK 204

RESULT 9
 SCF RAT STANDARD; PRT; 273 AA.
 AC P21581; Q9QWZ4; Q9Z2E7;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Klt ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
 DE cell growth factor) (MGF) (Hematopoietic growth factor KL).


```

CC      Name=1;
CC      IsoId=Q95N18-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q95N18-2; Sequence=VSP_006024;
CC      -1- PTM: A soluble form is produced by proteolytic processing of
CC      isoform 1 in the extracellular domain (by similarity).
CC      -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AY013712; MAG37434.1; -
DR      EMBL: AF23757; AAK7336.1; -
DR      InterPro: IPR003452; SCF.
DR      Pfam: PF02404; SCF, 1.
KW      Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW      Alternative splicing
FT      STGMAL 1
FT      CHAIN 25
FT      DOMAIN 26 274
FT      TRANSMEM 26 215
FT      DOMAIN 26 215
FT      TRANSMEM 216 238
FT      DOMAIN 216 238
FT      DISULFID 29 114
FT      DISULFID 68 164
FT      CARBOHYD 90 90
FT      CARBOHYD 97 97
FT      CARBOHYD 145 145
FT      CARBOHYD 196 196
FT      CARBOHYD 175 203
FT      VARSPLIC 175 203
FT      CONFLICT 65 65
FT      CONFLICT 171 171
FT      CONFLICT 268 274
FT      CONFLICT 274 274
SQ      SEQUENCE 274 AA; 31034 MW; 5AC1619014AE5E72 CRC64;
Query Match      81.0%; Score 859.5; DB 1; Length 274;
Best Local Similarity 83.3%; Pred. No. 1.3e-59;
Matches 170; Conservative 16; Mismatches 17; Indels 1; Gaps 1;
QY      1 MKKTQWILTCYLQLLRNPLVKTGICGNRTNNVQVTKLVANLPKQVMTLTKYVG 60
DB      1 MKKTQWILTCYLQLLRNPLVKTGICGNRTNNVQVTKLVANLPKQVMTLTKYVG 60
QY      61 MDVLPSCWISSEWVQLSDSLTDLKFSNISGLSNYSITDKLVNIYVDLVECVKENS 120
DB      61 MDVLPSCWISSEWVQLSDSLTDLKFSNISGLSNYSITDKLVNIYVDLVECVKENS 120
QY      121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDF-VVASETSDCVVSTLSEPKDSRVSV 179
DB      121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDF-VVASETSDCVVSTLSEPKDSRVSV 179
QY      121 ENVKSKSPKQDEPHFAPEDFRIFNRSIDALKDLLEVAKTSKCVLPSTLSEPKDSRVSV 180
DB      121 ENVKSKSPKQDEPHFAPEDFRIFNRSIDALKDLLEVAKTSKCVLPSTLSEPKDSRVSV 180
QY      180 TRPFMLPPVAASLRNDSSSNK 203
DB      180 TRPFMLPPVAASLRNDSSSNK 203
QY      181 TRPFMLPPVAASLRNDSSSNK 204
DB      181 TRPFMLPPVAASLRNDSSSNK 204
RESULT 11
SCF_MOUSE
ID      SCF_MOUSE STANDARD; PRT; 273 AA.
AC      P20826; P97332; Q62524; Q64222; Q921N5;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-MAY-1991 (Rel. 18, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast
DE      cell growth factor) (MGF) (Hematopoietic growth factor KL) (Steel
DE      factor).

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GN      KITLG OR KITL OR MGF OR SL OR SLF.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      (1)
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RC      STRAIN=MCB6F1;
RX      MEDLINE=9100423; PubMed=1698558;
RA      Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J.,
RA      Rauch C., March C.J., Boswell H.S., Gimpe S.D., Cosman D.,
RA      Williams D.E.;
RT      "Molecular cloning of mast cell growth factor, a hematopoietin that
RT      is active in both membrane bound and soluble forms.";
RL      Cell 63:235-243(1990).
RN      (2)
RP      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX      MEDLINE=9233001; PubMed=1378327;
RA      Huang E.J., Nocka K.H., Buck J., Besmer P.;
RT      "Differential expression and processing of two cell associated forms
RT      of the kit-ligand: KL-1 and KL-2.";
RL      Mol. Biol. Cell 3:349-362(1992).
RN      (3)
RP      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC      STRAIN=MCB6F1;
RX      MEDLINE=91160046; PubMed=1705866;
RA      Flanagan J.G., Chan D.C., Leder P.;
RT      "Transmembrane form of the kit ligand growth factor is determined by
RT      alternative splicing and is missing in the Sld mutant.";
RL      Cell 64:1025-1035(1991).
RN      (4)
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RX      MEDLINE=93012940; PubMed=1383087;
RA      Brannan C.I., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A.,
RA      Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A.,
RA      Copeland N.G.;
RT      "Developmental abnormalities in Steel17H mice result from a splicing
RT      defect in the steel factor cytoplasmic tail.";
RL      Genes Dev. 6:1832-1842(1992).
RN      (5)
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RC      STRAIN=C57BL/6J;
RX      MEDLINE=97002551; PubMed=8849898;
RA      Bedell M.A., Copeland N.G., Jenkins N.A.;
RT      "Multiple pathways for Steel regulation suggested by genomic and
RT      sequence analysis of the murine Steel gene.";
RL      Genetics 142:927-934(1996).
RN      (6)
RP      SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS PRO-193 AND SER-207.
RC      STRAIN=C3H/HeJ; TISSUE=Brain;
RX      MEDLINE=97032534; PubMed=8875893;
RA      Graw J., Loester J., Neuhaeuser-Klaus A., Pretsch W.,
RA      Schmitt-John T.;
RT      "Molecular analysis of two new Steel mutations in mice shows a
RT      transversion or an insertion.";
RL      Mamm. Genome 7:843-846(1996).
RN      (7)
RP      SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS SER-122; PRO-193 AND
RP      SER-207.
RC      STRAIN=102/E1 x C3H/HeJ;
RX      MEDLINE=98025115; PubMed=9360640;
RA      Graw J., Neuhaeuser-Klaus A., Pretsch W.;
RT      "Detection of a point mutation (A to G) in exon 5 of the murine Mgf
RT      gene defines a novel allele at the Steel locus with a weak
RT      phenotype.";
RL      Mutat. Res. 382:75-78(1997).
RN      (8)
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RC      STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,

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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kaskawa T., Saito R.,
 RA Kadota K., Matsumoto H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi G., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Futuro M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitlaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SER-207.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butcherfield Y.S.N., Krzyzanski M.I., Skalski D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RP SEQUENCE OF 1-270 FROM N.A. (ISOFORM 1), AND SEQUENCE OF 26-65.
 RX MEDLINE=91004221; PubMed=1698557;
 RA Huang E., Nocka K., Belier D.R., Chu T.Y., Buck J., Lahm H.W.,
 RA Wellner D., Leder P., Besmer P.;
 RT "The hematopoietic growth factor KL is encoded by the Sl locus and is
 the ligand of the c-kit receptor, the gene product of the w locus.";
 RL Cell 63:225-233(1990).
 RN [11]
 RP SEQUENCE OF 1-201 FROM N.A.
 RX MEDLINE=91004220; PubMed=1698556;
 RA Zeebo K.M., Williams D.A., Geisler E.N., Broudy V.C., Martin F.H.,
 RA Ackins H.L., Heu R.-Y., Birkett N.C., Okino K.J., Mardock D.C.,
 RA Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattaneach B.M.,
 RA Galli S.J., Stugs S.V.;
 RT "stem cell factor is encoded at the Sl locus of the mouse and is the
 ligand for the c-kit tyrosine kinase receptor.";
 RL Cell 63:213-224(1990).
 RN [12]
 RP SEQUENCE OF 26-53.
 RX MEDLINE=91004216; PubMed=1698554;
 RA Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A.,
 RA Cosman D., Anderson D., Lyman S.D., Williams D.E.,
 RT "Mast cell growth factor maps near the steel locus on mouse
 chromosome 10 and is deleted in a number of steel alleles.";
 RL Cell 63:175-183(1990).
 RN [13]
 RP PARTIAL SEQUENCE OF 26-78.
 RX MEDLINE=91004215; PubMed=1698553;
 RA Williams D.E., Eisenman J., Baird A., Rauch C., van Nese K.,
 RA March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S.,
 RA Burgess G.S., Cosman D., Lyman S.D.;
 RT "Identification of a ligand for the c-kit proto-oncogene.";

RL Cell 63:167-174(1990).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins.
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
 CC Also exists as a secreted soluble form (isoform 1 only) (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=KL-1;
 CC IsoId=P20826-1; Sequence=Displayed;
 CC Name=2; Synonyms=KL-2;
 CC IsoId=P20826-2; Sequence=VSP 006023;
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC isoform 1 in the extracellular domain.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M59915; AAA40095.1; -;
 DR EMBL; M57647; AAA39538.1; -;
 DR EMBL; S40534; AAA22555.2; -;
 DR EMBL; X68989; CAA48778.1; -;
 DR EMBL; U44724; -; NOT ANNOTATED_CDS.
 DR EMBL; U44725; AAC52447.1; -;
 DR EMBL; X95381; CAA64667.1; -;
 DR EMBL; X95382; CAA67698.1; -;
 DR EMBL; Y10287; CAA71329.1; -;
 DR EMBL; AK018777; BAB31402.1; -;
 DR EMBL; BC011322; AAH11322.1; -;
 DR EMBL; S40364; AAB22554.2; -;
 DR EMBL; M59912; AAA39539.1; -;
 DR PIR; A37934; A37934.
 DR PIR; S65801; S65801.
 DR MGI; MGI:965974; Kiti1.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 Query Match 80.6%; Score 85; DB 1; Length 273;
 Best Local Similarity 82.3%; Pred. No. 2.9e-59;
 Matches 167; Conservative 16; Mismatches 20; Indels 0; Gaps 0;
 QY 1 MKKTQWITTCIYLLDLPNPLVTEGICRNRYNNVADVTGLVNLPRKDWITTKYIPG 60
 DB 1 MKKTQWITTCIYLLDLPNPLVTEGICRNRYNNVADVTGLVNLPRKDWITTKYIPG 60
 QY 61 MVLPSHCWISMWVOLGSLTLDLDFKFSNISEGINSYIIDKLVNYDDIVECKENSS 120
 DB 61 MVLPSHCWISMWVOLGSLTLDLDFKFSNISEGINSYIIDKLVNYDDIVECKENSS 120
 QY 121 KDLKSPKSPSPRLTPEEFRIFNRSIDAFQFVASTSDCVVSTLSPKDSRVST 180
 DB 121 KDLKSPKSPSPRLTPEEFRIFNRSIDAFQFVASTSDCVVSTLSPKDSRVST 180
 QY 181 KPFMLPVAASGLRNDSSSSNSK 203
 DB 181 KPFMLPVAASGLRNDSSSSNSK 203
 RESULT 12
 SCF COTVA STANDARD; PRT; 287 AA.
 AC Q90314; Q90315;
 DT 28-FEB-2003 (Rel. 41, Created)

```

DT      28-FEB-2003 (Rel. 41, last sequence update)
DR      28-FEB-2003 (Rel. 41, last annotation update)
DE      kit ligand precursor (C-Kit ligand) (stem cell factor) (SCF) (Mast
DN      cell growth factor) (MGF).
OS      Kit ligand precursor (C-Kit ligand) (stem cell factor) (SCF) (Mast
OC      cell growth factor) (MGF).
OK      NCB1_TaxID=93934;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX      MEDLINE=96283808; PubMed=8679698;
RA      Pettite J.N., Kulik M.J.;
RT      "Cloning and characterization of cDNAs encoding two forms of avian
RL      stem cell factor."
RM      Biochim. Biophys. Acta 1307:149-151(1996).
RS      -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
RT      augment the proliferation of both myeloid and lymphoid
RC      hematopoietic progenitors in bone marrow culture. Mediates also
CC      cell-cell adhesion. Acts synergistically with other cytokines,
CC      probably interleukins (By similarity).
CC      -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC      -1- SUBUNIT: LOCATOR: Type I membrane protein (isoforms 1 and 2).
CC      Also exists as a secreted soluble form (isoform 1 only) (By
CC      similarity).
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=Q90314-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q90314-2; Sequence=VSP 006026;
CC      -1- PTM: A soluble form is produced by proteolytic processing of
CC      isoform 1 in the extracellular domain.
CC      -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL, U43078; AAC59933.1; -
DR      EMBL, U43079; AAC59934.1; -
DR      InterPro; IPR003452; SCF.
DR      Pfam; PF02404; SCF; 1.
KW      Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW      Alternative splicing.
FT      SIGNAL          1      25
FT      CHAIN           26      287
FT      DOMAIN          26      225
FT      TRANSMEM        226      246
FT      DOMAIN          247      287
FT      DISULFID         29      117
FT      DISULFID         68      167
FT      CARBOHYD         100      100
FT      CARBOHYD         106      106
FT      CARBOHYD         149      149
FT      CARBOHYD         178      178
FT      CARBOHYD         200      200
FT      CARBOHYD         206      206
FT      VARSPLIC         179      213
FT      -----
FT      POTENTIAL.
FT      KIT LIGAND.
FT      EXTRACELLULAR (POTENTIAL).
FT      POTENTIAL.
FT      CYTOPLASMIC (POTENTIAL).
FT      BY SIMILARITY.
FT      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      DSRVAVTKTISPPVAASLSLRDSIGSNTSSNSNK -> E
FT      (in isoform 2).
FT      /FTId=VSP 006026.
SQ      SEQUENCE      287 AA;  32455 MW;  AB81AEAF422A702E CRC64;
Query Match      53.8%; Score 570.5; DB 1; Length 287;
Best Local Similarity 55.1%; Pred. No. 3,1e-37;
Matches 114; Conservative 37; Mismatches 51; Indels 5; Gaps 3;
1 MKKDTWTLLTCTIYDLDLLEPNLVKTEGICRRNVTNNVQDVKLVANLEPKDYMTLTKYVG 60

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Db	1	MDVLPESHCMISEMVAVQSDSLTDLLDKF---SNISEGSLSNYSIIIDKLVINVDVLECYKE	117
Qy	61	MDVLPESHCMISEMVAVQSDSLTDLLDKF---SNISEGSLSNYSIIIDKLVINVDVLECYKE	117
Db	61	MDSLPNHCMLHLMVPEFSRSLHNLLQKFVDISDMSDVLSNYSIIINNLFTIINDLMACLAIF	120
Qy	118	NSKSD-LKSKRSKPPPLPLTPEPEFRIRNRSIDAKDPVAVSETSDCVASSTL-SPEKRS	175
Db	121	DKNDDFKENHLYEEDRFIPENPFRLPNKRTIEVYKEFPADSLDKNDCLMPSTVETPEPDS	180
Qy	176	RVSVTKEPMLPPVAASSLRNDSSSSNS	202
Db	181	RVAVTKTISFEPVAASSLRNDSIGSNT	207
RESULT	13		
SCF	CHICK		
ID	SCF	CHICK	STANDARD: PRT: 287 AA.
AC	009108.		
DT	01-FEB-1995	(Rel. 31, Created)	
DT	01-FEB-1995	(Rel. 31, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	Kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast cell growth factor) (MGF).		
GN	KITLG OR SCF.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
NCBI	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=93273244; PubMed=7684722;		
RA	Zhou J., Ohtaki M., Sakurai M.;		
RT	"Sequence of a cDNA encoding chicken stem cell factor.";		
RL	Gene 127:269-270(1993).		
CC	-I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).		
CC	-I- SUBUNIT: Homodimer, non-covalently linked (Probable).		
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).		
CC	-I- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.		
CC	-I- PFM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).		
CC	-I- SIMILARITY: BELONGS TO THE SCF FAMILY.		
CC	-----		
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CC	-----		
DR	EMBL; D13516; BAA02733.1; -		
DR	PIR; J06637; J06637.		
DR	InterPro; IPR003452; SCF.		
DR	Pfam; PF02404; SCF.1.		
KW	Growth factor; Glycoprotein; Transmembrane; signal; Cell adhesion.		
FT	SIGNAL	1 25	POTENTIAL.
FT	CHAIN	26 287	KIT LIGAND.
FT	DOMAIN	26 225	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	226 246	POTENTIAL.
FT	DOMAIN	247 287	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	29 117	BY SIMILARITY.
FT	DISULFID	68 167	BY SIMILARITY.
FT	CARBOHYD	100 100	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	149 149	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	200 200	N-LINKED (GLCNAC. . .) (POTENTIAL).

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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:59:08 ; Search time 24.3526 Seconds
(without alignments)
2204.073 Million cell updates/sec

Title: US-09-224-683-46

Perfect score: 1061

Sequence: 1 MKKTQTWILTCIYLQLLFLN.....AASSLRNDSSSSNKYIYLI 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp_rvrvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	855	80.6	208	11	Q64384
2	509	48.0	123	11	Q61854
3	480	45.2	160	11	Q6C9K1
4	327	30.8	271	13	Q9YGP2
5	273.5	25.8	270	13	Q8AYN7
6	116.5	11.0	1637	5	Q8ITM4
7	116.5	11.0	1711	5	Q8MWP2
8	116.5	11.0	1713	5	Q8MWP1
9	116.5	11.0	1716	5	Q8MWP2
10	100	9.4	3072	12	Q92645
11	97.5	9.2	1480	5	Q19545
12	97	9.1	1447	16	Q9PQJ8
13	96.5	9.1	1458	3	Q96VK6
14	96.5	9.1	1458	3	Q9P884
15	94.5	8.9	576	11	Q62970
16	94	8.9	906	5	Q8IEF0

17	94	8.9	1238	12	Q9EMP3	Q9emp3 amacta moo
18	94	8.9	1816	5	Q81095	Q81095 caenorhabdi
19	93.5	8.8	579	11	Q99KM2	Q99KM2 mus musculu
20	93.5	8.8	722	11	Q8BZT8	Q8BZT8 mus musculu
21	92.5	8.7	164	16	P71021	P71021 bacillus su
22	92.5	8.7	512	16	Q9CGA7	Q9CGA7 lactococcus
23	92	8.7	188	5	Q9VRK2	Q9VRK2 dirosophila
24	92	8.7	2907	5	Q8IC71	Q8IC71 plasmodium
25	91.5	8.6	496	16	Q8D221	Q8D221 wiggleswort
26	91.5	8.6	976	2	Q54222	Q54222 staphylococ
27	91	8.6	317	5	Q9VTY2	Q9VTY2 dirosophila
28	91	8.6	317	5	Q8SX88	Q8SX88 dirosophila
29	91	8.6	422	12	Q911L4	Q911L4 white spot
30	91	8.6	1107	3	Q12271	Q12271 saccharomyc
31	90.5	8.5	254	11	Q9J116	Q9J116 rattus norv
32	90.5	8.5	616	17	Q26384	Q26384 methanobact
33	90	8.5	937	10	Q9MAL4	Q9MAL4 arabidopsis
34	90	8.5	967	5	Q8IKR7	Q8IKR7 plasmodium
35	90	8.5	1218	12	Q8VAV7	Q8VAV7 white spot
36	90	8.5	1219	12	Q911B1	Q911B1 white spot
37	90	8.5	1219	12	Q8QTD0	Q8QTD0 white spot
38	90	8.5	1501	3	Q96VL9	Q96VL9 boctrytis ci
39	88.5	8.3	228	16	Q9XC73	Q9XC73 salmoneila
40	88.5	8.3	464	16	Q8EQ50	Q8EQ50 oceanobacil
41	88.5	8.3	941	10	Q9SINO	Q9SINO arabidopsis
42	88.5	8.3	963	10	Q8GVE9	Q8GVE9 arabidopsis
43	88.5	8.3	968	10	Q93XG8	Q93XG8 hydrilla ve
44	88.5	8.3	1056	16	Q8RE77	Q8RE77 fusobacteri
45	88.5	8.3	1570	5	Q9U0H8	Q9U0H8 plasmodium

ALIGNMENTS

RESULT 1

Q64384 PRELIMINARY; PRT; 208 AA.
ID Q64384;
AC Q64384;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Mast cell growth factor (Fragment).
GN KITL OR MGF OR SL OR KL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92330001; PubMed=1378327;
RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
RT "Differential expression and processing of two cell associated forms
of the kit-ligand: KL-1 and KL-2".
RL Mol. Biol. Cell 3:349-362(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160046; PubMed=1705866;
RA Flanagan J.G., Chan D.C., Leder P.;
RT "Transmembrane form of the kit ligand growth factor is determined by
alternative splicing and is missing in the slt mutant".
RL Cell 64:1025-1035(1991).
DR EMBL: 540536; AAA92556.2; -
DR EMBL: M64262; AAA9378.1; -
DR MGD; MGI:96974; K1L1.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
FT NON TER 208
SQ SEQUENCE 208 AA; 23222 MW; C74DD63956EB817 CRC64;

Query Match 80.6%; Score 855; DB 11; Length 208;
Best Local Similarity 82.3%; Pred. No. 1.7e-61;
Matches 167; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

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QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRYNNVQVTKLVANLPRDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICGNPVTDVVKDITKLVANLPNDYMITLNVYAG 60
QY 61 MVLPSHCWISSENVVQSLDLDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLYECVENS 120
DB 61 MVLPSHCWLRDWNVQLSLTLTLDFKFSNISSEGLSNYSIIDKLVNIIVDDLYECVENS 120
QY 121 KOLKSKFSPPEPLFTPEEFRIENRSIDAFKDFVVASSTSDCVSSSTLSPKXSVST 180
DB 121 KNIKSPKRPETRSFTPEEFRIENRSIDAFKDFVVASSTSDCVSSSTLSPKXSVST 180
QY 181 KPFMLPPVAASSLRNDSSSSNSK 203
DB 181 KPFMLPPVAASSLRNDSSSSNSK 203

RESULT 2
ID 061854 PRELIMINARY; PRT; 123 AA.
AC 061854;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DB Mast cell growth factor.
GN KITL OR MGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97032534; PubMed=8875893;
RA Graw J., Loester J., Neuhäuser-Klaus A., Pretsch W., Schmitt-John T.;
RT "Molecular analysis of two new Steel mutations in mice shows a
RT transversion or an insertion."
RL Mamm. Genome 7:843-846(1996).
DR EMBL; X95379; CAAG4666.1; -.
DR MGI; MGI:96974; Kitl.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
SQ SEQUENCE 123 AA; 13892 MW; A872B455A85D642 CRC64;

Query Match
Best Local Similarity 48.0%; Score 509; DB 11; Length 123;
Matches 98; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRYNNVQVTKLVANLPRDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICGNPVTDVVKDITKLVANLPNDYMITLNVYAG 60
QY 61 MVLPSHCWISSENVVQSLDLDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLYECVENS 120
DB 61 MVLPSHCWLRDWNVQLSLTLTLDFKFSNISSEGLSNYSIIDKLVNIIVDDLYECVENS 120
QY 121 K 121
DB 121 K 121

RESULT 3
ID 08C9K1 PRELIMINARY; PRT; 160 AA.
AC 08C9K1;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DB Kit ligand (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
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RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK041961; BAC31113.1; -.
FT NON_TER 160
SQ SEQUENCE 160 AA; 17492 MW; B12AC581346AAE6D CRC64;

Query Match
Best Local Similarity 45.2%; Score 480; DB 11; Length 160;
Matches 92; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 6 TWILTCIYQLLEFNPVKTGICRNRYNNVQVTKLVANLPRDYMITLKYVPGMDVLP 65
DB 46 TWILTCIYQLLEFNPVKTGICGNPVTDVVKDITKLVANLPNDYMITLNVYAGMDVLP 105
QY 66 SHCWISSENVVQSLDLDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLYECVENS 119
DB 106 SHCWLRDWNVQLSLTLTLDFKFSNISSEGLSNYSIIDKLVNIIVDDLYECVENS 159

RESULT 4
ID 09YGP2 PRELIMINARY; PRT; 271 AA.
AC 09YGP2;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DB Steel factor.
DE Steel factor.
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxId=8296;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=99299573; PubMed=10370116;
RA Parichy D.M., Stigson M., Voss S.R.;
RT "Genetic analysis of steel and the P-G/W/versican-encoding gene AXPg as
RT candidates for the white (d) pigmentation mutant in the salamander
RT Ambystoma mexicanum."
RL Dev. Genes Evol. 209:349-356(1999).
DR EMBL; AF119044; AAD17253.1; -.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
SQ SEQUENCE 271 AA; 30075 MW; 876977ABF7D53EB4 CRC64;

Query Match
Best Local Similarity 30.8%; Score 327; DB 13; Length 271;
Matches 83; Conservative 29; Mismatches 78; Indels 22; Gaps 6;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRYNNVQVTKLVANLPRDYMITLKYVPG 56
DB 1 MKKTQWILTCIYQLLEFNPVKTGICGNPVTDVVKDITKLVANLPNDYMITLNVYAG 53
QY 57 YVPGMDVLPVPSHCWISSENVVQSLDLDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLYECV 116
DB 54 YVPMPSLPKQCVYIWMHAKXSNISGLIHKFPANTSO---NYSIMSNITLALHGRNOLA 110
QY 117 -----ENSSKDLKSKSPPEPLFTPEEFRIENRSIDAFKDFVVASSTSDCVS-STLSP 171
DB 111 SOLIDNEBFIIDPFYDGE---FVPEKEYKYVTITLTKAIHKMDDDSTCELPVTEETP 167
QY 172 EKDSRVSTKRPMLPVAASSLRNDSSSSNSK 203
DB 168 LSDLPVGVTKPSAKFSFMPSSSRKOREGIPNAK 199
```


Best Local Similarity 23.0%; Pred. No. 0.93;
Matches 35; Conservative 41; Mismatches 57; Indels 19; Gaps 6;

QY 31 NRYTNVNVKVTQKLVAN-----LPKDYMTLTKYVPGM-DVLSHCWISGMV---Q 76
Db 1223 HKINNNLKDITHIVINDNNTLOEQNRITVNELOKIKQIKVSDVFTHTNINYSQOILINYSQ 1282
QY 77 LSDSLDLDLDFKFNISSEGLSN--YSIIDKLVINVD--DLVECVKENSXKOLKKSFKSPSP 132
Db 1283 AQNSFPNIFPMKFNINNDINSKRYNVOKITEIINSYDIIN-YKNKNIDIVQOQFNIIQO 1341
QY 133 RLFTPEEFRIFRNSIDAFKDPVAVSETSDCV 164
Db 1342 QLTMTETQLNHKIKONINHFKEYESHQTSIV 1373

RESULT 9

Q8MMH2 PRELIMINARY; PRT; 1716 AA.
AC Q8MMH2;
DT C1-OCT-2002 (T-EMBLrel. 22, Created)
DT C1-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT C1-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Reticulocyte binding protein homolog 4.
GN RH4.
OS Plasmodium falciparum (isolate NF54).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5843;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22030722; PubMed=12034462;
RA Kaneo O., Mu J.-B., Tsuboi T., Su X.-Z., Torii M.;
RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
RT protein homologous to the Plasmodium vivax reticulocyte binding
RT protein.";
RL Mol. Biochem. Parasitol. 121:275-278 (2002).
DR EMBL; AF432854; AAM47192.1;
SQ SEQUENCE 1716 AA; 205846 MW; 2A3DAC35B6FE226 CRC64;

Query Match 11.0%; Score 116.5; DB 5; Length 1716;
Best Local Similarity 23.0%; Pred. No. 0.93;
Matches 35; Conservative 41; Mismatches 57; Indels 19; Gaps 6;

QY 31 NRYTNVNVKVTQKLVAN-----LPKDYMTLTKYVPGM-DVLSHCWISGMV---Q 76
Db 1220 HKINNNLKDITHIVINDNNTLOEQNRITVNELOKIKQIKVSDVFTHTNINYSQOILINYSQ 1279
QY 77 LSDSLDLDLDFKFNISSEGLSN--YSIIDKLVINVD--DLVECVKENSXKOLKKSFKSPSP 132
Db 1280 AQNSFPNIFPMKFNINNDINSKRYNVOKITEIINSYDIIN-YKNKNIDIVQOQFNIIQO 1338
QY 133 RLFTPEEFRIFRNSIDAFKDPVAVSETSDCV 164
Db 1339 QLTMTETQLNHKIKONINHFKEYESHQTSIV 1370

RESULT 10

Q92645 PRELIMINARY; PRT; 3072 AA.
AC Q92645;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Polyprotein.
OS Clover yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
OC Potyvirus.
OX NCBI_TaxID=12198;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=No.30;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=No.30;

RX MEDLINE=97456254; PubMed=9311568;
RA Takahashi Y., Takahashi T., Uyeda I.;
RT "A cDNA clone to clover yellow vein potyvirus genome is highly
RT infectious.";
RL Virus Genes 14:235-243 (1997).
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
DR EMBL; AB011819; BA25147.1; -.

DR MEROPS; C04.008; -.
DR Interpro; IPR001410; DEAD.
DR Interpro; IPR001650; Helicase_C.
DR Interpro; IPR001730; Peptidase_C4.
DR Interpro; IPR001456; Peptidase_C6.
DR Interpro; IPR001592; Polypeptide.
DR Interpro; IPR002540; Polypeptide.
DR Interpro; IPR007095; RNA pol_D5_P5.
DR Interpro; IPR007094; RNA pol_PSVir.
DR Pfam; PF00271; Helicase_C_1.
DR Pfam; PF00863; Peptidase_C4_1.
DR Pfam; PF00851; Peptidase_C6_1.
DR Pfam; PF00767; Polypeptide_1.
DR Pfam; PF01577; Polypeptide_1.
DR Pfam; PF00680; RNA dep. RNA pol. 1.
DR PRINTS; PR00966; NIAPOTPTASE.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC_C; 1.
DR PROSITE; PS05057; RDRP POSITIVE; 1.
DR PROSITE; PS05051; RDRP VIRAL; 1.
KW ATP-binding; Coat protein; Helicase; Hydrolase.
SQ SEQUENCE 3072 AA; 348727 MW; F3EBA84BD96D385A CRC64;

Query Match 9.4%; Score 100; DB 12; Length 3072;
Best Local Similarity 21.5%; Pred. No. 39;
Matches 46; Conservative 38; Mismatches 72; Indels 58; Gaps 10;

QY 23 VKTEGICR-----NRYTNVNVKVTQKLVAN--LPKDYMTLTKYVGMVLPKHCW-- 69
Db 639 IAKDGYCHINIFPAMLVNVSSEKSDPTKVRDQIMPK-----LGQWPTMLDVATAVCWYL 693
QY 70 -----ISEWVQLSDSLDLDLDFKFNISSEGLSNYSIIDKLVINVDLVECVKEN 118
Db 694 TWPFDTISAEPLRILVHKSLTMAVLDSYGSISIG--YVYLK--ANIVSOLIFASDD 748
QY 119 SSKDLKSKSPSPRLFTPEEFRIFRNSIDAFKDPVAVSETSDCVSSTLSPKDSRVS 178
Db 749 LESDLK-----FYRVGKSLTG--QVIQPTK-MLISSIVRPQMEKII 789
QY 179 VTKPFML-----PVAASLRNDSSSSNSKITYL 207
Db 790 NEPPVLVLAMQSPSVLLALFNLSASLEKAVEWL 823

RESULT 11

Q19545 PRELIMINARY; PRT; 1490 AA.
AC Q19545;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical 168.5 kDa protein.
GN F18C5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;

RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Fulton L.;
RT "The sequence of C. elegans cosmid F18C5."
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U29097; AAA68411.1; -.
DR WormPep; F18C5.3; CE02652.
KW Hypothetical protein.
SQ SEQUENCE 1490 AA; 168480 MW; 89FF7AD689A9E668 CRC64;

Query Match 9.1%; Score 97.5; DB 5; Length 1490;
Best Local Similarity 24.4%; Pred. No. 27;
Matches 54; Conservative 28; Mismatches 82; Indels 57; Gaps 9;

QY 20 NPLVTEGICRNRVTNNKQVTKLVANLPKDYMITLKYPGMDVLPSCWISSEWVQLSD 79
DB 732 NGAVKAE--CPKAKGNAPPEMOMHGRIVSPAGIQWLAFFRVVNEH--PSAKAVQ--- 784
QY 80 SLTDLDFKSNISEGLSNYSIID-----KLVINVDLVECVKENSCKDLKSKFS 129
DB 785 RVSDLLSKFAG---GLKDNEISLDSQLGYIFKSLTSDIOKLEVERKNGQKDEKQGR 841
QY 130 PEERLFPPEFRFRL--FNRSIDAFKDPVVASFSDCVSSTLSPEK-----DSRVSVTK 182
DB 842 PESCLILPAPQRIKAGMSKVIRSRDHVFA--EFFVLLFSSLLKEKFDLSDSMSVRLNP 900
QY 183 FM-----LPPVAASSR 194
DB 901 FVKIILDCFPKYEKILSCSMRALSSMIOQLPAIANSQR 941

RESULT 12
Q9PQJ8 PRELIMINARY; PRT; 1447 AA.
AC 09PQJ8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein U0293.
GN U0293.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.J., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
urealyticum."
RL Nature 407:757-762(2000).
DR EMBL; AB002126; AAF30702.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1447 AA; 167444 MW; A22A194FF79A0289 CRC64;

Query Match 9.1%; Score 97; DB 16; Length 1447;
Best Local Similarity 29.7%; Pred. No. 29;
Matches 41; Conservative 29; Mismatches 38; Indels 30; Gaps 9;
QY 17 LLENPLVKT-----EGICNRVTNNKQVTKLVANLPKDYMITLKYPGMDVLP 67
DB 17 LLENPLVKT-----EGICNRVTNNKQVTKLVANLPKDYMITLKYPGMDVLP 67

DB 351 IILNAPDKIEIIRNTSNIINNAKQODIKK---QIDKIYLLIKKVLQTOFLNRSK 407
QY 68 CWISEWVQLSDSLTDLDK--FSN-----ISEGLSNY---SIIDKLVINVD-----LVE 113
DB 408 AKTS--VKINETITLIDSLFANGEIITLISNTLSNMFSSNLAKIINVEDQNSLIK 465
QY 114 CYKE--NSSKDLKSKFS 129
DB 466 PVVERFIISSNDLKTILKT 483

RESULT 13
Q96VK6 PRELIMINARY; PRT; 1498 AA.
AC 096VK6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ABC transporter protein.
GN ATRE.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG096;
RA Andrade A.C., Braam C., Haas H., De Waard M.A.;
RT "ABC transporters and resistance to azole fungicides in the ima
mutants of Aspergillus nidulans."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AJ309280; CAC42216.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR001063; Ribosomal_L22.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
DR PROSITE; PS00464; RIBOSOMAL_L22; 1.
KW ATP-binding; Transport.
SQ SEQUENCE 1498 AA; 167675 MW; EBB9FF3F46110FEB CRC64;

Query Match 9.1%; Score 96.5; DB 3; Length 1498;
Best Local Similarity 20.4%; Pred. No. 33;
Matches 57; Conservative 35; Mismatches 88; Indels 99; Gaps 10;

QY 17 LLENPLVKT-----EGICNRVTNNKQVTKLVANLPKDYMITLK-----YVRG----- 60
DB 263 LMFSAIARPRNRRLGVSRSKQYAEHRDV--VMAMIGLSHTINTRVGNDPIRGVSGGERK 320
QY 61 -----MDVLPSCWIS-----MVQLSDSLTD 83
DB 321 RVSIATATISQAPLQCDWNSGTGLDSANALEFCXKALAMSKTGTSTACVAITQASQAYD 380
QY 84 LLDKSNISEGLSNY--SIIDKLVINVDLVECVKENSCKDLKSKFSPEPLF----- 135
DB 381 VFDKTVLVEGRQIYFGNTKDAKKFFVDWGFCPEROTADPLTSLTSPAEHLVPRYEG 440
QY 136 ----TPSEFRIFNR-----SIDAKFPVVASFSDCVSS- 167
DB 441 RVPCPDPDEPAAAMKSEERAKLMAIEEYEROYPIGSPYDAFVARKAMSKORVNSP 500
QY 168 -TLSEPKDSRVSVTKPFMLPVAASLRDSSSSNSKYI 205
DB 501 YTIISTWQVSLCVARGF-----QRLKQDFSLTTTSLI 532

RESULT 14
Q9P884

ID	Q9P884	PRELIMINARY;	PRT; 1498 AA.
AC	Q9P884;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	ABC transporter protein.		
GN	ATRE.		
OS	<i>Emericella nidulans</i> (<i>Aspergillus nidulans</i>).		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;		
OC	Eurotiota; Trichocomaceae; Emericella.		
OX	NCBI_TaxID=162425;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-MG096;		
RA	Andrade A.C., Van Nistelrooy J.G.M., Haas H., De Waard M.A.;		
RT	"ABC transporters and resistance to azole fungicides in the ima		
RT	mutants of <i>Aspergillus nidulans</i> ."		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.		
DR	EMBL; AJ276241; CAB76823.1; -		
DR	InterPro; IPR003593; AAA_ATPase.		
DR	InterPro; IPR003439; ABC_TRANSPORTER.		
DR	InterPro; IPR000847; HTH_LYER.		
DR	InterPro; IPR001063; Ribosomal_L22.		
DR	Pfam; PF00005; ABC_tran; 2.		
DR	PfDom; PDD00006; ABC_transporter; 2.		
DR	SMART; SM00382; AAA; 2.		
DR	PROSITE; PS00211; ABC_TRANSPORTER; 1.		
DR	PROSITE; PS00044; HTH_LYSR_FAMILY; 1.		
DR	PROSITE; PS00464; RIBOSOMAL_L22; 1.		
KW	ATP-binding; Transport.		
SO	SEQUENCE 1498 AA; 167706 MW; AABDEA3FFDLAEEB CRC64;		

RESULT	15			
062970				
ID	Q62970	PRELIMINARY;	PRT;	576 AA.
AC	Q62970;			
DT	01-NOV-1996	(TrEMBLrel. 01, Created)		
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)		
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)		
DE	Apolipoprotein B (Fragment).			
GN	APOB.			
OS	Rattus norvegicus (Rat).			
OC	Eulaliaota, Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

RC	TISSUE=Liver;					
RA	Shimmin L.C.;					
Rt	"Rattus norvegicus partial apob sequence.";					
RL	Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.					
DR	EMBL; U53873; AAA98613.1; -.					
KW	Lipoprotein.					
FT	NON_TER	1	1			
FT	NON_TER	576	576			
SQ	SEQUENCE	576 AA;	66762 MW;	PF649CCAA69AA07A	CRC64;	
<hr/>						
Query Match	8.9%;		Score 94.5;	DB 11;	Length 576;	
Best Local Similarity	24.1%;		Pred. No. 16;			
Matches 45;	Conservative 35;	Mismatches 64;	Indels 43;	Gaps 7		

```

QY      32 RYVNNKQDVTKVALNPDKDMYTLCKY-----VPGMDVPSHCMISEMVQSD-----79
Db      89 RISVIERKRYVNMHLIEDPKTEKINFRIYAVELIEKY-EVDROIQVMDKSIELAHR 147

QY      80 -SLTDLDDKFSNISBGLSNYSIIDKLVNIYVDLVECVKENSCKDL-----KKSF 127
Db      148 YSLSEPLQGLSTNVLQOIEIKQDYDKLVGFIDDTVEIMIKAVSFKNIIELNRILDMVSVKKL 207

QY      128 KSEEPRLFTPE-----EEFRLENST-----DAFKDFFVASSTSDCVSSTLSPE 172
Db      208 KAFDYHQFVDKTNKSIRETORINAEIOALELPORTEALKLWEDPFKTT---VSNLSLEKL 264

QY      173 KDSRVSU 179
Db      265 KDTKVTV 271

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Search completed: February 5, 2004, 15:07:28
Job time : 26.3526 secs

PA (AMGE-) AMGEN INC.
XX Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX MPI: 1991-119233/17.
XX N-PSDB; AAQ11542.
XX
XX New naturally-occurring polypeptide stem cell factor analogues -
PT have haematopoietic biological activity of stem cell factor and
PT are used to treat eg leukopenia, AIDS, nerve damage and
PT infertility
XX
XX Disclosure; Fig 42; 127pp; English.
XX
XX The SCF has the ability to stimulate growth of primitive
CC progenitors including early hematopoietic progenitor cells and non-
CC hematopoietic stem cells such as neural stem cells and primordial
CC germ stem cells. The product may be used in a pharmaceutical
CC compen. for treating, in a mammal, leukopenia, thrombocytopenia,
CC anaemia, AIDS, neoplasia, nerve damage, infertility and
CC intestinal damage.
CC See also AAR11708, AAQ11509-Q11543.
XX
SQ Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 12; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQDTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQDTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
QY 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASFSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASFSDCVSSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMALPALFSLIIGFAGALYWKCR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMALPALFSLIIGFAGALYWKCR 240
QY 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 273
DB 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 273

RESULT 2
AAR20647
ID AAR20647 standard; Protein; 273 AA.
XX
XX AAR20647;
AC
XX
DT 25-MAR-2003 (updated)
DT 30-MAR-1992 (first entry)
XX
DE Human mast cell growth factor.
XX
XX hMGF-2.4; hematopoietin; interleukin; IL-3; c-kit oncogene;
KM proliferation.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..25
FT Peptide /label= signal
FT 26..210
FT Region /label= "extracellular"
FT /note= "Claimed polypeptide"
FT Region 211..237

FT
FT Region /label= transmembrane
FT 238..273
FT /label= intracellular

PN WO9200376-A.
XX
XX 09-JAN-1992.
PD
XX
XX 14-JUN-1991; 91WO-US04274.
PF
XX
XX 25-JUN-1990; 90US-0543264.
PR 10-AUG-1990; 90US-0565840.
PR 28-AUG-1990; 90US-0574152.
PR 21-SEP-1990; 90US-0586073.
PR 12-JUN-1991; 91US-0713715.
XX

PA (IMMV) IMMUNEX CORP.
XX
XX Williams DE, Lyman S;
PI
XX
XX MPI: 1992-041558/05.
DR
XX
XX N-PSDB; AAQ20845.

PT New isolated DNA encoding human mast cell growth factor - useful in
PT stimulating proliferation of haematopoietic cells with growth factor,
PT to treat haemolytic and hypoproliferative anaemias
XX
XX Claim 10; Fig 4; 59pp; English.

XX This human MGF has a mature extracellular region of 185 amino acids.
CC There is a second form of hMGF (see AAQ20844) resulting from an
CC alternative mRNA splicing event which deletes an exon encoding an
CC additional 28 amino acids beginning at amino acid 148 of the mature
CC protein. MGF is the ligand for the protein receptor expression product
CC of the c-kit proto-oncogene. MGF can be used to augment the
CC activity of other cytokines. It can influence early lymphoid or
CC myeloid development. See also AAQ20842-3 and AAQ22204-7.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQDTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQDTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
QY 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASFSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASFSDCVSSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMALPALFSLIIGFAGALYWKCR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMALPALFSLIIGFAGALYWKCR 240
QY 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 273
DB 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 273

RESULT 3
AAR83978
ID AAR83978 standard; Protein; 273 AA.
XX
XX AAR83978;
AC
XX
DT 25-MAR-2003 (updated)

DT 15-MAY-1996 (first entry)
 XX Human stem cell factor derived from HT1080 fibrosarcoma cell line.
 XX
 KM Stem cell factor; progenitor; hematopoiesis; SCF; anaemia;
 KM thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
 KM transplant; neoplasia; myelosuppression; bone marrow; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= sig_peptide
 FT Protein 26..248
 FT /label= mat_SCF
 XX
 PN EP676470-A1.
 XX
 PD 11-OCT-1995.
 XX
 PF 04-OCT-1990; 95EP-0105391.
 XX
 PR 01-OCT-1990; 90US-0589701.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90MO-US05548.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 PA Bosselman RA, Martin FH, Suggs SV, Zsebo KM;
 PI WPI; 1995-346090/45.
 DR N-PSDB; AAT04890.
 XX
 PT New stem cell factor polypeptide(s) - for stimulating the growth of
 PT primitive progenitor cells, esp. for treating disorders involving
 PT blood cells
 XX
 PS Claim 9; Fig 42; 127pp; English.
 XX
 XX AAR83978 is a human stem cell factor (SCF) derived from the HT1080
 CC fibrosarcoma cell line. Non-naturally occurring SCF and C-terminally
 CC truncated polypeptides, having amino acid sequences sufficiently
 CC duplicative of naturally occurring SCF, stimulate growth of primitive
 CC progenitors such as haematopoietic progenitor cells, neural stem
 CC cells and primordial germ stem cells. The peptides can be used in a
 CC composition for treating leucopenia, anaemia or thrombocytopenia,
 CC for enhancing engraftment of bone marrow during transplantation or
 CC for bone marrow recovery after chemotherapy or radiation-induced bone
 CC marrow aplasia or myelosuppression. They can also be used for
 CC treating neoplasia, nerve damage, infertility, intestinal damage or
 CC myeloproliferative disorders. Antibodies may be raised against the
 CC peptides for use in detection or neutralisation of SCF in serum. SCF
 CC may be useful for the treatment of AIDS and severe combined
 CC immunodeficiency (SCID) states alone or in combination with other
 CC factors such as IL-7.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 XX
 SQ Sequence 273 AA;
 Query Match 100.0%; Score 1397; DB 16; Length 273;
 Best Local Similarity 100.0%; Pred.No.3.3e-133; Indels 0; Gaps 0;
 Matches 273; Conservative 0; Mismatches 0;
 QY 1 MKKTQWTILTCIYQLLLFNPVLTGECINRVTNNVQDVTKLVANLPKQDMITLTKVPG 60
 DB 1 MKKTQWTILTCIYQLLLFNPVLTGECINRVTNNVQDVTKLVANLPKQDMITLTKVPG 60
 QY 61 MDVLPSCWISSEWVQSLDILDLKFSNISBSGLSVYIIDKLVINIVDLVECVKENS 120
 DB 61 MDVLPSCWISSEWVQSLDILDLKFSNISBSGLSVYIIDKLVINIVDLVECVKENS 120
 61 MDVLPSCWISSEWVQSLDILDLKFSNISBSGLSVYIIDKLVINIVDLVECVKENS 120

QY 121 KDLKKSFKSPPERLFTPEEPFRIFNRSIDAFKDFVVASSETSDCVVSTLSPBKSRVSVT 180
 DB 121 KDLKKSFKSPPERLFTPEEPFRIFNRSIDAFKDFVVASSETSDCVVSTLSPBKSRVSVT 180
 QY 181 KPFMLPPVAASSLRNDSSSNRKANPPGDSLSHMAALPALFSLIIGFAPGALYMKKR 240
 DB 181 KPFMLPPVAASSLRNDSSSNRKANPPGDSLSHMAALPALFSLIIGFAPGALYMKKR 240
 QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREPOEV 273
 DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREPOEV 273
 RESULT 4
 AAW27607
 ID AAW27607 standard; Protein; 273 AA.
 XX
 AC AAW27607;
 XX
 DT 28-APR-1998 (first entry)
 XX
 DE Human recombinant stem cell factor protein.
 XX
 KM Stem cell factor; SCF; mast cell growth factor; MCGF; Steel factor;
 KM SF; SLF; analogue; treatment; haematopoietic factor; progenitor cell;
 KM pigmentation disorder; haematopoietic disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= leader sequence
 FT Protein 26..274
 FT /note= "mature full length stem cell factor protein"
 XX
 PN WO9738101-A1.
 XX
 PD 16-OCT-1997.
 XX
 PF 03-APR-1997; 97MO-US05541.
 XX
 PR 05-APR-1996; 96US-0628428.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Lu HS;
 XX
 DR WPI; 1997-512718/47.
 XX
 PT Stem cell factor analogue N10D or N10D/N10D - useful to treat
 PT pigmentation disorder, AIDS, nerve damage, infertility, intestinal
 PT damage or haematopoietic disorder
 XX
 PS Claim 2; Fig 1; 42pp; English.
 XX
 XX This sequence represents a membrane bound form of a human recombinant
 CC stem cell factor (SCF). Stem cell factors are also known as mast cell
 CC growth factors (MCGF) or Steel factors (SF or SLF) are haematopoietic
 CC factors which act on haematopoietic progenitor cells. Analogues of a
 CC wild type SCF sequence have been constructed (see AAW27605 and AAW27606)
 CC which have increased biological activity and stability compared to
 CC unmodified SCF and can be used treat pigmentation disorders, e.g.
 CC vitiligo, acquired immunodeficiency syndrome, nerve damage, infertility,
 CC intestinal damage or a haematopoietic disorder, e.g. leucopenia,
 CC thrombocytopenia or anaemia, enhance bone marrow engraftment during
 CC transplantation or bone marrow recovery following radiation, chemical or
 CC chemotherapeutic, induced bone marrow aplasia or myelosuppression,
 CC sensitive cells to chemotherapy or mobilise peripheral blood progenitor
 CC cells. It can also be used in an in vitro haematopoietic cell, preferably
 CC bone marrow or peripheral blood progenitor cell, culture medium, where
 CC the cells are optionally subsequently transfected with exogenous DNA.
 XX
 SQ Sequence 273 AA;

PD 19-JUN-2001.
 XX 24-MAY-1995; 95US-0449653.
 XX
 PR 10-APR-1991; 91US-0684535.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 PR 21-DEC-1993; 93US-0172329.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSSELMAN R A.
 PA (SUGS/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
 FI
 XX
 DR WPI; 2001-407312/43.
 DR N-PSDB; AAS10461.
 XX
 PT Increasing the number of early haematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell
 PT factor -
 XX
 PS Example 3; Fig 42; 210pp; English.
 XX
 CC The present sequence represents human stem cell factor (SCF). The cDNA
 CC encoding this sequence is isolated from the H1080 fibrosarcoma cell
 CC line. The sequence is described in an invention relating to novel stem
 CC cell factors, the polynucleotides encoding them and methods for
 CC producing the stem cell factors. The methods involve increasing the
 CC number of early haematopoietic progenitor cells in human peripheral
 CC blood by administering a haematopoietically effective human stem cell
 CC factor polypeptide. The methods are useful for the treatment of blood
 CC disorders, including myelofibrosis, myelocytosis, osteopetrosis,
 CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
 CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
 CC anaemia, malaria, vitamin B12 and folic acid deficiency,
 CC hypopigmentation disorders i.e. piebaldism and viral induced disorders,
 CC including AIDS.
 XX
 SQ Sequence 273 AA;
 Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWMLTCTIYQLLFPNPLVKTGICRNRVTNNKDVTKLVANLPKDYMITLTKVPG 60
 DB 1 MKKTQWMLTCTIYQLLFPNPLVKTGICRNRVTNNKDVTKLVANLPKDYMITLTKVPG 60
 QY 61 MDVLPSCWISSEMVVQSLDLDLDFKSNISEGLSNYSIIDKLVIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEMVVQSLDLDLDFKSNISEGLSNYSIIDKLVIYVDLVECKENSS 120
 QY 121 KDLLKSKFSPPEPLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
 DB 121 KDLLKSKFSPPEPLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
 QY 181 KPFLPVAASSLRNDSSSNRKAQNPBGDSSLHMAAMALPALFSLITGAFGALYWKRR 240
 DB 181 KPFLPVAASSLRNDSSSNRKAQNPBGDSSLHMAAMALPALFSLITGAFGALYWKRR 240
 QY 241 QPSLTRAVENTQINEEDNEISMLOEKERREFOEV 273
 DB 241 QPSLTRAVENTQINEEDNEISMLOEKERREFOEV 273

ID AAB98357 standard; Protein; 273 AA.
 XX
 AC AAB98357;
 XX
 DT 21-AUG-2001 (first entry)
 XX
 DE Human SCF protein SEQ ID NO:49.
 XX
 KM Stem cell factor; SCF, stem cell factor receptor; blood cell disorder;
 KM gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US6207454-B1.
 XX
 PD 27-MAR-2001.
 XX
 PF 31-DEC-1998; 98US-0224681.
 XX
 PR 21-DEC-1993; 93US-0172329.
 PR 24-MAY-1995; 95US-0449653.
 PR 12-JAN-1998; 98US-0005893.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
 FI
 XX
 DR WPI; 2001-366062/38.
 XX
 XX Enhancing efficiency of transfer of polynucleotide into a target
 PT mammalian cell in vitro, involves exposing cell that expresses a stem
 PT cell factor receptor to stem cell factor, and introducing
 PT polynucleotide into cell in vitro -
 XX
 PS Example 3; Fig 16; 210pp; English.
 XX
 CC The present invention describes a method for enhancing (B) the
 CC efficiency of transfer of a polynucleotide (I) into a target mammalian
 CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
 CC factor (SCF) receptor to a biologically active SCF, its analogue or
 CC fragment, which induces cell proliferation, and introducing (I) to (II)
 CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)
 CC into the cell. The method is useful for enhancing the efficiency of the
 CC transfer of a polynucleotide into a target mammalian cell in vitro.
 CC The method is useful in gene therapy techniques. AAH41301 to AAH41364
 CC and AAB98351 to AAB98390 represent sequences used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 273 AA;
 Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWMLTCTIYQLLFPNPLVKTGICRNRVTNNKDVTKLVANLPKDYMITLTKVPG 60
 DB 1 MKKTQWMLTCTIYQLLFPNPLVKTGICRNRVTNNKDVTKLVANLPKDYMITLTKVPG 60
 QY 61 MDVLPSCWISSEMVVQSLDLDLDFKSNISEGLSNYSIIDKLVIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEMVVQSLDLDLDFKSNISEGLSNYSIIDKLVIYVDLVECKENSS 120
 QY 121 KDLLKSKFSPPEPLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
 DB 121 KDLLKSKFSPPEPLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
 QY 181 KPFLPVAASSLRNDSSSNRKAQNPBGDSSLHMAAMALPALFSLITGAFGALYWKRR 240
 DB 181 KPFLPVAASSLRNDSSSNRKAQNPBGDSSLHMAAMALPALFSLITGAFGALYWKRR 240

Db 181 KPFMLPVAASSLRNDSSSSNRKAKNPDDSLHWAAMALPALFSLITGFAGALYWKRR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273
 Db 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273

RESULT 8
 ID AAB98367 standard; Protein; 273 AA.
 AC AAB98367;
 XX
 DT 21-AUG-2001 (first entry)
 XX
 DE Human SCF protein sequence SEQ ID NO:61.
 XX
 KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US6207454-B1.
 PD 27-MAR-2001.
 XX
 PF 31-DEC-1998; 98US-0224681.
 XX
 PR 21-DEC-1993; 93US-0172329.
 PR 24-MAY-1995; 95US-0449653.
 PR 12-JAN-1998; 98US-0005893.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX
 PA (AMGE-) AMGEN INC.
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 DR WPI; 2001-366062/38.
 DR N-PSDB; AAH41344.
 XX
 PT Enhancing efficiency of transfer of polynucleotide into a target
 PT mammalian cell in vitro, involves exposing cell that expresses a stem
 PT cell factor receptor to stem cell factor, and introducing
 PT polynucleotide into cell in vitro -
 XX
 PS Claim 17; Fig 42; 210pp; English.
 XX
 CC The present invention describes a method for enhancing (E) the
 CC efficiency of transfer of a polynucleotide (I) into a target mammalian
 CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
 CC factor (SCF) receptor to a biologically active SCF, its analogue or
 CC fragment, which induces cell proliferation, and introducing (I) to (II)
 CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)
 CC into the cell. The method is useful for enhancing the efficiency of the
 CC transfer of a polynucleotide into a target mammalian cell in vitro.
 CC The method is useful in gene therapy techniques. AAH41301 to AAH41364
 CC and AAB98351 to AAB98390 represent sequences used in the exemplification
 CC of the present invention.
 CC
 SQ Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILITCTYLOLLFNPLVKTGICGRNRYTNVKNVYKLVANLPRDVMITTKYVPG 60
 DB 1 MKKTQWILITCTYLOLLFNPLVKTGICGRNRYTNVKNVYKLVANLPRDVMITTKYVPG 60

QY 61 MDVLPSCWISSEMVVQLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYDDLVECVKENS 120
 Db 61 MDVLPSCWISSEMVVQLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYDDLVECVKENS 120
 QY 121 KDLKSKFSPEPRLLTPPEPFRIENRSDAFKDFVAVASETDCVVSSTLSPEKDSRVSYT 180
 Db 121 KDLKSKFSPEPRLLTPPEPFRIENRSDAFKDFVAVASETDCVVSSTLSPEKDSRVSYT 180
 QY 181 KPFMLPVAASSLRNDSSSSNRKAKNPDDSLHWAAMALPALFSLITGFAGALYWKRR 240
 Db 181 KPFMLPVAASSLRNDSSSSNRKAKNPDDSLHWAAMALPALFSLITGFAGALYWKRR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273
 Db 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273

RESULT 9
 ID AAU02460 standard; Protein; 273 AA.
 AC AAU02460;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
 XX
 KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 KW HT1080 fibrosarcoma.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..25
 FT /label= Signal_peptide
 FT Protein 26..273
 FT /label= Mature_SCF
 XX
 PN US6207417-B1.
 PD 27-MAR-2001.
 XX
 PF 07-JUN-1995; 95US-0482918.
 XX
 PR 21-DEC-1993; 93US-0172329.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 DR WPI; 2001-298941/31.
 DR N-PSDB; AAS04124.
 XX
 PT Novel nucleic acids encoding stem cell factor useful for treating
 PT disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
 PT disease, Kala azar, anaemia and septicemia -
 XX
 PS Example 5; Fig 42A-42C; 209pp; English.
 XX
 CC The present sequence representing human SCF (stem cell factor) protein
 CC is isolated from the HT1080 fibrosarcoma cell line. The present invention
 CC relates to novel stem cell factors (AAU02453-AAU02458, AAU02461) and
 CC the polynucleotides encoding them. SCF stimulate primitive progenitor
 CC cells including early haematopoietic progenitor cells. The invention also

describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides (AA04081-AA04117) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency, CC pyridoxine deficiency, and hypopigmentation disorders such as piebaldism and vitiligo.

Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLOLLFNPVKTGICRNVTNNVKDTLVANLPKDYMITLKYVPG 60
1 MKKTQWILTCIYLOLLFNPVKTGICRNVTNNVKDTLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYLOLLFNPVKTGICRNVTNNVKDTLVANLPKDYMITLKYVPG 60
QY 61 MDVLPCHCWISEMVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
61 MDVLPCHCWISEMVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPCHCWISEMVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSYT 180
121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSYT 180
DB 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSYT 180
QY 181 KPEFMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMLPAFLSLIGAFAGALYMKR 240
181 KPEFMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMLPAFLSLIGAFAGALYMKR 240
DB 181 KPEFMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMLPAFLSLIGAFAGALYMKR 240
QY 241 QPSLTRAVENIQINEEDNEISMLQEKERERFQEV 273
241 QPSLTRAVENIQINEEDNEISMLQEKERERFQEV 273
DB 241 QPSLTRAVENIQINEEDNEISMLQEKERERFQEV 273

RESULT 10

ID AAU02766 standard; Protein; 273 AA.

AC AAU02766;

XX 29-AUG-2001 (first entry)

XX Human SCF protein isolated from the HT1080 fibrosarcoma cell line.

KW Human: stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW HT1080 fibrosarcoma.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..25 /label= Signal_peptide

FT Protein 26..273 /label= Mature_SCF

XX US6218148-B1.

XX 17-APR-2001.

XX 21-DEC-1993; 93US-0172329.

XX 25-NOV-1992; 92US-0982255.

XX 16-OCT-1989; 89US-0422383.

XX 11-JUN-1990; 90US-0537198.

XX 24-AUG-1990; 90US-0573616.

XX 01-OCT-1990; 90US-0589701.

XX (AMGE-) AMGEN INC.

PA Zsebo KM, Bosseiman RA, Suggs SV, Martin FH;

XX WPI; 2001-281051/29.

XX N-PSDB; AA04224.

PT Isolated DNA sequence, encoding polypeptide product useful for

XX stimulating growth of early haematopoietic progenitor cells -

XX Example 5; Fig 42A-42C; 167pp; English.

CC The present sequence representing human SCF (stem cell factor) protein
CC is isolated from the HT1080 fibrosarcoma cell line. The present
CC invention relates to novel stem cell factors
CC (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides
CC encoding them. SCF stimulate primitive progenitor cells including early
CC haematopoietic progenitor cells. The invention also describes SCF
CC peptides (AAU02777-AAU02794) and the oligonucleotides
CC (AA04182-AA04218) used in the isolation of human and rat SCF
CC sequences. The polynucleotide encoding SCF is useful for producing
CC SCF and useful in gene therapy. It is useful for treating disorders
CC involving blood cells such as myelofibrosis, metastatic carcinoma,
CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
CC sarcoidosis, military tuberculosis, disseminated fungus disease,
CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
CC pyridoxine deficiency, and hypopigmentation disorders such as
CC piebaldism and vitiligo.

Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLOLLFNPVKTGICRNVTNNVKDTLVANLPKDYMITLKYVPG 60
1 MKKTQWILTCIYLOLLFNPVKTGICRNVTNNVKDTLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYLOLLFNPVKTGICRNVTNNVKDTLVANLPKDYMITLKYVPG 60
QY 61 MDVLPCHCWISEMVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
61 MDVLPCHCWISEMVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPCHCWISEMVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSYT 180
121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSYT 180
DB 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSYT 180
QY 181 KPEFMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMLPAFLSLIGAFAGALYMKR 240
181 KPEFMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMLPAFLSLIGAFAGALYMKR 240
DB 181 KPEFMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMLPAFLSLIGAFAGALYMKR 240
QY 241 QPSLTRAVENIQINEEDNEISMLQEKERERFQEV 273
241 QPSLTRAVENIQINEEDNEISMLQEKERERFQEV 273
DB 241 QPSLTRAVENIQINEEDNEISMLQEKERERFQEV 273

RESULT 11

ID AAB73567 standard; Protein; 273 AA.

AC AAB73567;

XX 07-AUG-2001 (first entry)

XX Human SCF protein isolated from the HT1080 fibrosarcoma cell line.

KW Human: stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW HT1080 fibrosarcoma.

```

OS Homo sapiens.
XX Key Location/Qualifiers
FH Protein 1..25
FT Protein /label= signal_peptide
FT Protein 26..273
FT Protein /label= Mature_SCF
XX
XX US6204363-B1.
XX
XX 20-MAR-2001.
XX
XX 25-NOV-1992; 92US-0982255.
XX
XX 10-APR-1991; 91US-0684535.
XX 16-OCT-1989; 89US-0422383.
XX 11-JUN-1990; 90US-0537198.
XX 24-AUG-1990; 90US-0573616.
XX 01-OCT-1990; 90US-0589701.
XX
XX (AMGE-) AMGEN INC.
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-256683/26.
XX N-PSDB; AAH23901.
XX
XX New stem cell factor polypeptides and their analogs which stimulate
XX growth of early hematopoietic progenitors, useful for treating aplastic
XX anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
XX disease
XX
XX Claim 7; Fig 42A-42C; 166pp; English.
XX
XX The present sequence representing human SCF (stem cell factor) protein
XX is isolated from the HT1080 fibrosarcoma cell line. The present
XX invention relates to novel stem cell factors
XX (AAH23561-AAH73568, AAH73571-AAH73576) and the polynucleotides
XX encoding them. SCF stimulate primitive progenitor cells including early
XX hematopoietic progenitor cells. The invention also describes SCF
XX peptides (AAH73578-AAH73597) and the oligonucleotides
XX (AAH23859-AAH23895) used in the isolation of human and rat SCF
XX sequences. The polynucleotide encoding SCF is useful for producing
XX SCF and useful in gene therapy. It is useful for treating disorders
XX involving blood cells such as myelofibrosis, metastatic carcinoma,
XX acute leukemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
XX sarcoidosis, military tuberculosis, disseminated fungus disease,
XX fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX pyridoxine deficiency, and hypopigmentation disorders such as
XX piebaldism and vitiligo.
XX
XX Sequence 273 AA:
SQ

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Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MKKTQWTLITCYLQLLFPNPLVKTGICRRNVTNNVDYTKLVANLPRDYMITLKYVG 60
DB 1 MKKTQWTLITCYLQLLFPNPLVKTGICRRNVTNNVDYTKLVANLPRDYMITLKYVG 60
QY 61 MOVLPESHCMISEWVQLSDSLTDLDKFSNISISGLSNYSITDKLVNIIVDVLVECVKENS 120
DB 61 MOVLPESHCMISEWVQLSDSLTDLDKFSNISISGLSNYSITDKLVNIIVDVLVECVKENS 120
QY 121 KDLKSFKSPPEPLFTPEEPFRIFNRSIDAFKDFVVAASEPDCVASTLSPEDSRVSVT 180
DB 121 KDLKSFKSPPEPLFTPEEPFRIFNRSIDAFKDFVVAASEPDCVASTLSPEDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSNRKAKNPQDSSSLHMAAMALPALFSLIIFAGALYMKR 240
DB 181 KPFMLPPVAASSLRNDSSSNRKAKNPQDSSSLHMAAMALPALFSLIIFAGALYMKR 240

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QY 241 QPSTRAVENIOINEDNEISMLQEKREPOEV 273
DB 241 QPSTRAVENIOINEDNEISMLQEKREPOEV 273

```

```

RESULT 12
ID AAB96941 standard; Protein; 273 AA.
XX AAB96941;
XX
XX 13-JUL-2001 (first entry)
XX
XX Human stem cell factor SEQ ID NO: 48.
XX
XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
XX gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
XX neurological damage; intestinal damage; infertility; AIDS; SCID;
XX severe combined immunodeficiency.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Protein 1..25
FT Protein /label= signal_peptide
FT Protein 26..273
FT Protein /label= mature_stem_cell_factor
XX
XX US6207802-B1.
XX
XX 27-MAR-2001.
XX
XX 09-NOV-1994; 94US-0336728.
XX
XX 25-NOV-1992; 92US-0982255.
XX 16-OCT-1989; 89US-0422383.
XX 11-JUN-1990; 90US-0537198.
XX 24-AUG-1990; 90US-0573616.
XX 01-OCT-1990; 90US-0589701.
XX
XX (AMGE-) AMGEN INC.
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-353108/37.
XX N-PSDB; AAF89102.
XX
XX Novel isolated non-human mammalian stem cell factor polypeptide
XX stimulating growth of early haematopoietic progenitor cells, useful for
XX treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
XX sarcoidosis
XX
XX Disclosure; Fig 15D; 209pp; English.
XX
XX The present invention provides the protein and coding sequences of
XX mammalian stem cell factors (SCFs). These are capable of stimulating the
XX growth of early haematopoietic progenitor cells, neural stem cells and
XX primordial germ stem cells. The sequences are useful in the treatment of
XX leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
XX nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
XX and intestinal damage, infertility, AIDS and severe combined
XX immunodeficiency (SCID). The present sequence is an SCF described in the
XX invention.
XX
XX Sequence 273 AA:
SQ

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Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MKKTQWTLITCYLQLLFPNPLVKTGICRRNVTNNVDYTKLVANLPRDYMITLKYVG 60

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Db 1 MKKTQTWILTCIYLQLLFNPVLTGEGICRRVTNNVDYTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCWISSEMVVQLSDSLTDLDKFSNISEGLSNYSIIDKLVINIYDDLVECYKENS 120
 Db 61 MDVLPSCWISSEMVVQLSDSLTDLDKFSNISEGLSNYSIIDKLVINIYDDLVECYKENS 120
 QY 121 KDLKKSFKSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 Db 121 KDLKKSFKSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 QY 181 KPFLMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
 Db 181 KPFLMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
 QY 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273
 Db 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273

RESULT 13

AAB96942 standard; Protein; 273 AA.
 AAB96942;

13-JUL-2001 (first entry)

Human stem cell factor SEQ ID NO: 49.

Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 neurological damage; intestinal damage; infertility; AIDS; SCID;
 severe combined immunodeficiency.

Homo sapiens.

US6207802-B1.

27-MAR-2001.

09-NOV-1994; 94US-0336728.

25-NOV-1992; 92US-0982255.

16-OCT-1989; 89US-0422383.

11-JUN-1990; 90US-0537198.

24-AUG-1990; 90US-0573616.

01-OCT-1990; 90US-0589701.

(AMGE-) AMGEN INC.

Zsebo KM, Bosseman RA, Suggs SV, Martin FH;

WPI; 2001-353108/37.

Novel isolated non-human mammalian stem cell factor polypeptide
 stimulating growth of early haematopoietic progenitor cells, useful for
 treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
 sarcoïdosis -
 Example 3; Fig 16; 209pp; English.

The present invention provides the protein and coding sequences of
 mammalian stem cell factors (SCFs). These are capable of stimulating the
 growth of early haematopoietic progenitor cells, neural stem cells and
 primordial germ stem cells. The sequences are useful in the treatment of
 leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
 nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
 and intestinal damage, infertility, AIDS and severe combined
 immunodeficiency (SCID). The present sequence is an SCF described in the
 invention.

Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQTWILTCIYLQLLFNPVLTGEGICRRVTNNVDYTKLVANLPKDYMITLKYPVG 60
 Db 1 MKKTQTWILTCIYLQLLFNPVLTGEGICRRVTNNVDYTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCWISSEMVVQLSDSLTDLDKFSNISEGLSNYSIIDKLVINIYDDLVECYKENS 120
 Db 61 MDVLPSCWISSEMVVQLSDSLTDLDKFSNISEGLSNYSIIDKLVINIYDDLVECYKENS 120
 QY 121 KDLKKSFKSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 Db 121 KDLKKSFKSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 QY 181 KPFLMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
 Db 181 KPFLMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
 QY 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273
 Db 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273

RESULT 14

AAB96952 standard; Protein; 273 AA.

13-JUL-2001 (first entry)

Human stem cell factor SEQ ID NO: 61.

Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 neurological damage; intestinal damage; infertility; AIDS; SCID;
 severe combined immunodeficiency.

Homo sapiens.

US6207802-B1.

27-MAR-2001.

09-NOV-1994; 94US-0336728.

25-NOV-1992; 92US-0982255.

16-OCT-1989; 89US-0422383.

11-JUN-1990; 90US-0537198.

24-AUG-1990; 90US-0573616.

01-OCT-1990; 90US-0589701.

(AMGE-) AMGEN INC.

Zsebo KM, Bosseman RA, Suggs SV, Martin FH;

WPI; 2001-353108/37.

N-PSDB; AAF89104.

Novel isolated non-human mammalian stem cell factor polypeptide
 stimulating growth of early haematopoietic progenitor cells, useful for
 treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
 sarcoïdosis -
 Example 3; Fig 42; 209pp; English.

XX The present invention provides the protein and coding sequences of
 CC mammalian stem cell factors (SCFs). These are capable of stimulating the
 CC growth of early haematopoietic progenitor cells, neural stem cells and
 CC primordial germ stem cells. The sequences are useful in the treatment of
 CC leukemias, haematopoietic disorders, aplastic anaemia, paroxysmal
 CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
 CC and intestinal damage, infertility, AIDS and severe combined
 CC immunodeficiency (SCID). The present sequence is an SCF described in the
 CC invention.

XX SQ Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 23; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVDYTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVDYTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPBHCWISBMVQVLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
 DB 61 MDVLPBHCWISBMVQVLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
 QY 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 DB 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 QY 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 240
 DB 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273
 DB 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273

RESULT 15

ABG95642 ID ABG95642 standard; Protein; 273 AA.

AC ABG95642;

DT 05-DEC-2002 (first entry)

DE Human SCF protein from HT1080 fibrosarcoma cell line.

XX Stem cell factor; SCF; blood-forming system; blood cell disorder;
 KW haematopoietic system; metastatic carcinoma; acute leukaemia;
 KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
 KW refractory erythroblastic anaemia; military tuberculosis; cytostatic;
 KW disseminated fungus disease; haematopoietic; tuberculostatic;
 KW antianaemic; antifungal; antimarial; dermatological; human;
 KW HT1080 fibrosarcoma cell line.

OS Homo sapiens.

XX EP1241258-A2.

PD 18-SEP-2002.

PF 04-OCT-1990; 2002EP-0008587.

XX 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90WO-US05548.

PR 01-OCT-1990; 90US-0589701.

PR 04-OCT-1990; 90EP-0310899.

PR 04-OCT-1990; 95EP-0105391.

PA (AMGE-) AMGEN INC.

XX Zeebo KM, Suggs SV, Bosselman RA, Martin FH;
 XX WPI; 2002-684093/74.
 DR N-PSDB; ABS73859.

XX Production of a human stem cell factor (SCF) polypeptide for treating
 PT disorders involving blood cells, such as leukaemia, comprises culturing
 PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
 PT encoding the human SCF -

XX Example 16; Fig 42; 120pp; English.

XX The present invention relates to novel stem cell factors (SCFs),
 CC polynucleotide sequences encoding the SCFs, and methods of producing
 CC them. SCFs are involved in the blood-forming (haematopoietic)
 CC system in mammals, particularly humans. The method of the invention
 CC is useful for the production of human SCF. The stem cell factors are
 CC useful to treat disorders involving blood cells e.g. metastatic
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
 CC lymphoma, refractory erythroblastic anaemia, military tuberculosis,
 CC disseminated fungus disease, malaria, and vitiligo. The present
 CC sequence represents human SCF protein isolated from the HT1080
 CC fibrosarcoma cell line.

SQ Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 23; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVDYTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVDYTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPBHCWISBMVQVLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
 DB 61 MDVLPBHCWISBMVQVLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
 QY 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 DB 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 QY 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 240
 DB 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273
 DB 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273

Search completed: February 5, 2004, 15:05:14
 Job time : 40.1074 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2004, 15:03:24 ; Search time 14.2893 Seconds
(without alignments)
808.360 Million cell updates/sec

Title: US-09-224-683-61

Perfect score: 1397
Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISWLQKREPEQEV 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1397	100.0	273	1	US-08-220-379B-2
2	1397	100.0	273	2	US-08-628-428-9
3	1397	100.0	273	3	US-08-482-918-49
4	1397	100.0	273	3	US-08-482-918-61
5	1397	100.0	273	3	US-09-224-681-49
6	1397	100.0	273	3	US-09-224-681-61
7	1397	100.0	273	3	US-08-336-728A-48
8	1397	100.0	273	3	US-08-336-728A-49
9	1397	100.0	273	3	US-08-336-728A-61
10	1392	99.6	273	3	US-08-482-918-48
11	1392	99.6	273	3	US-09-224-681-48
12	1381	98.9	273	3	US-08-482-918-50
13	1381	98.9	273	3	US-09-224-681-50
14	1378	98.6	273	3	US-08-336-728A-50
15	1265	90.6	248	2	US-08-955-848A-82
16	1232.5	88.2	266	3	US-08-482-918-57
17	1232.5	88.2	266	3	US-09-224-681-57
18	1232.5	88.2	266	3	US-08-336-728A-57
19	1231	88.1	245	3	US-08-482-918-63
20	1231	88.1	245	3	US-09-224-681-63
21	1231	88.1	245	3	US-08-336-728A-63
22	1202.5	86.1	274	3	US-08-336-728A-52
23	1180.5	84.5	274	3	US-08-482-918-51
24	1180.5	84.5	274	3	US-09-224-681-51
25	1180.5	84.5	274	3	US-08-336-728A-51
26	1179.5	84.4	271	3	US-08-482-918-52
27	1179.5	84.4	271	3	US-09-224-681-52

28	1178.5	84.4	274	3	US-08-336-728A-53	Sequence 53, Appl
29	1173	84.0	273	3	US-08-482-918-53	Sequence 53, Appl
30	1173	84.0	273	3	US-09-224-681-53	Sequence 53, Appl
31	1158	82.9	273	3	US-08-482-918-42	Sequence 42, Appl
32	1158	82.9	273	3	US-09-224-681-42	Sequence 42, Appl
33	1158	82.9	273	3	US-08-336-728A-42	Sequence 42, Appl
34	1158	82.9	273	3	US-08-336-728A-54	Sequence 54, Appl
35	1157	82.8	273	1	US-08-220-379B-6	Sequence 6, Appl
36	1157	82.8	273	3	US-08-482-918-55	Sequence 55, Appl
37	1157	82.8	273	3	US-09-224-681-55	Sequence 55, Appl
38	1157	82.8	273	3	US-08-336-728A-55	Sequence 55, Appl
39	1151	82.4	273	3	US-08-482-918-54	Sequence 54, Appl
40	1151	82.4	273	3	US-09-224-681-54	Sequence 54, Appl
41	1144	81.9	273	1	US-08-341-456A-11	Sequence 11, Appl
42	1144	81.9	273	2	US-08-478-414A-11	Sequence 11, Appl
43	1144	81.9	273	3	US-08-325-240A-11	Sequence 11, Appl
44	1144	81.9	273	3	US-08-898-982-11	Sequence 11, Appl
45	1144	81.9	273	4	US-09-371-261-11	Sequence 11, Appl

ALIGNMENTS

```
RESULT 1
US-08-220-379B-2
; Sequence 2, Application US/08220379B
; Patent No. 5525708
; GENERAL INFORMATION:
; APPLICANT: No. 5525708ka, Karl
; APPLICANT: Lobell, Robert B
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,379B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Cytowed/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9090
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: cleavage site
; LOCATION: 164..165
; US-08-220-379B-2

Query Match      100.0%   Score 1397;   DB 1;   Length 273;
Best Local Similarity 100.0%;   Pred. No. 2.9e-134;   Indels 0;   Gaps 0;
Matches 273;   Conservative 0;   Mismatches 0;

QY      1 MKKTQWILTCIYLQLLFNPLVKTEGI CRNRVTNNVQDVTKLVANLPKQWITLKYPVG 60
DB      1 MKKTQWILTCIYLQLLFNPLVKTEGI CRNRVTNNVQDVTKLVANLPKQWITLKYPVG 60
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QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIVDLVECVKENS 120
QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLSHWAAMALPALFSLIIGFAGALYMKR 240
DB 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLSHWAAMALPALFSLIIGFAGALYMKR 240
QY 241 OPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273
DB 241 OPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273

RESULT 2
US-08-628-428-9
; Sequence 9, Application US/08628428
; Patent No. 5885962
; GENERAL INFORMATION:
; APPLICANT: Lu, Hsieng
; TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,428
; FILING DATE: 05-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..273
; OTHER INFORMATION: /note="NOTE: Mature full length
; OTHER INFORMATION: 1-248 SCF protein begins at amino acid 26; amino acid 1-25
; OTHER INFORMATION: include Met and leader sequences for membrane band form of hu
; OTHER INFORMATION: recombinant SCF."
US-08-628-428-9

Query Match 100.0%; Score 1397; DB 2; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRRNRYNNVKDVTKLVANLPKQYMITLKYPVG 60
DB 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRRNRYNNVKDVTKLVANLPKQYMITLKYPVG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIVDLVECVKENS 120

QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLSHWAAMALPALFSLIIGFAGALYMKR 240
DB 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLSHWAAMALPALFSLIIGFAGALYMKR 240
QY 241 OPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273
DB 241 OPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273

RESULT 3
US-08-482-918-49
; Sequence 49, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
; APPLICANT: Bosseman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-49

Query Match 100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRRNRYNNVKDVTKLVANLPKQYMITLKYPVG 60
DB 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRRNRYNNVKDVTKLVANLPKQYMITLKYPVG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIVDLVECVKENS 120
QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180

QY	181	KPFMLPVAASSLRNDSSSSNNKANKNPEDSSLLHMAAMALPALFSLITIGFAFGALYWKRR	240
Db	181	KPFMLPVAASSLRNDSSSSNNKANKNPEDSSLLHMAAMALPALFSLITIGFAFGALYWKRR	240
QY	241	QPSLTRAVENTIQINEEDNEISMLOEKEREFEQEV	273
Db	241	QPSLTRAVENTIQINEEDNEISMLOEKEREFEQEV	273

RESULT 4
US-08-482-918-61

; Sequence 61, Application US/08482918
; Patent No.6207417
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482, 918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: 1linear
; MOLECULE TYPE: protein
; US-08-482-918-61

QY	Query Match	100.0%;	Score 1397;	DB 3;	Length 273;
QY	Best Local Similarity	100.0%;	Pred. No. 2.9e-134;		
Db	Matches 273;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	MKKTOTWITCYIYQLLLFNPLVKTGEGIRNRYTNVVKVTKYVAMLPKDYMTLLKYVP	60
Db	1	MKKTQWILTCYIQLLLFNPLVKTGICRNRVTNVKQDTKLVAMLPKDYMTLLKYVP	60
QY	61	MDVLPSHCWISSEWVQVLSLDLTDLDKFSNISSEGLSNYSIIDKLAVNIIVDLVECVKENS	120
Db	61	MDVLPSHCWISSEWVQVLSLDLTDLDKFSNISSEGLSNYSIIDKLAVNIIVDLVECVKENS	120
QY	121	KDLKSKFSPPEPLFTPEEPFRIENRSIDAQDFVAASETSDCVSSTSPKDSRVSVT	180
Db	121	KDLKSKFSPPEPLFTPEEPFRIENRSIDAQDFVAASETSDCVSSTSPKDSRVSVT	180
QY	181	KPFMLPVAASSLRNDSSSSNNKANKNPEDSSLLHMAAMALPALFSLITIGFAFGALYWKRR	240
Db	181	KPFMLPVAASSLRNDSSSSNNKANKNPEDSSLLHMAAMALPALFSLITIGFAFGALYWKRR	240

```

Db      241  QPSLTRAVENTIOINEDNEISMLQEKEREFQEV 273
        |||||||
        241  QPSLTRAVENTIOINEDNEISMLQEKEREFQEV 273

RESULT 5
US-09-224-681-49
: Sequence 49, Application US/09224681
: Patent No. 6207454
: GENERAL INFORMATION:
: APPLICANT: Zsebo, Krisztina M.
: APPLICANT: Bosseiman, Robert A.
: APPLICANT: Sugars, Sidney H.
: APPLICANT: Martin, Francis H.
: TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
: TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
: NUMBER OF SEQUENCES: 104
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/224,681
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/005,893
: FILING DATE: 12-JAN-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/449,653
: FILING DATE: 24-MAY-1995
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/982,255
: FILING DATE: 25-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/589,701
: FILING DATE: 01-OCT-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/573,616
: FILING DATE: 24-AUG-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/537,198
: FILING DATE: 11-JUN-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/422,383
: FILING DATE: 16-OCT-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Clough, David W.
: REGISTRATION NUMBER: 36,107
: REFERENCE/DOCKET NUMBER: 01017/35199
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX:
: INFORMATION FOR SEQ ID NO: 49:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 273 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-09-224-681-49

```

Query Match 100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKYVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKYVG 60

QY 61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDIVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDIVECVKENS 120

QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 180

QY 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
DB 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240

QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFEV 273

RESULT 6
US-09-224-681-61
Sequence 61, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-61

Query Match 100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKYVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKYVG 60

QY 61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDIVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDIVECVKENS 120

QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 180

QY 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
DB 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240

QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFEV 273

RESULT 7
US-08-336-728A-48
Sequence 48, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255

FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-48

Query Match 100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYLLFNPVLYKTEGICRNKRVNNKVDYKLVANLPKDYMTITLKYPG 60
DB 1 MKKTQWILTCIYLLFNPVLYKTEGICRNKRVNNKVDYKLVANLPKDYMTITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIVDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIVDDLVCEKENS 120
QY 121 KDLKSKFSPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVST 180
DB 121 KDLKSKFSPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVST 180
QY 181 KPMLPVVAASLRNDSSSNRKAQNPQDSSLHMAAMALPALFSLIIGFAGALYWK 240
DB 181 KPMLPVVAASLRNDSSSNRKAQNPQDSSLHMAAMALPALFSLIIGFAGALYWK 240
QY 241 QPSLTRAVENIOINEEDNEISMLQEKERFQEV 273
DB 241 QPSLTRAVENIOINEEDNEISMLQEKERFQEV 273

RESULT 8
US-08-336-728A-49
Sequence 49, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Sugs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-49

Query Match 100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYLLFNPVLYKTEGICRNKRVNNKVDYKLVANLPKDYMTITLKYPG 60
DB 1 MKKTQWILTCIYLLFNPVLYKTEGICRNKRVNNKVDYKLVANLPKDYMTITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIVDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIVDDLVCEKENS 120
QY 121 KDLKSKFSPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVST 180
DB 121 KDLKSKFSPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVST 180
QY 181 KPMLPVVAASLRNDSSSNRKAQNPQDSSLHMAAMALPALFSLIIGFAGALYWK 240
DB 181 KPMLPVVAASLRNDSSSNRKAQNPQDSSLHMAAMALPALFSLIIGFAGALYWK 240
QY 241 QPSLTRAVENIOINEEDNEISMLQEKERFQEV 273
DB 241 QPSLTRAVENIOINEEDNEISMLQEKERFQEV 273

RESULT 9
US-08-336-728A-61
Sequence 61, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Sugs, Sidney V.

APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/569,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/557,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-61

Query Match 100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQTWILTCIYQLLLFNPLVKTGICRRVTNNVQVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQTWILTCIYQLLLFNPLVKTGICRRVTNNVQVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPBHCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIYVDLVECKENSS 120
DB 61 MDVLPBHCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIYVDLVECKENSS 120
QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLIIGFAFGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLIIGFAFGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273

RESULT 10
US-08-482-918-48
Sequence 48, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Krieszina M.
APPLICANT: Bosseleman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-48

Query Match 99.6%; Score 1392; DB 3; Length 273;
Best Local Similarity 99.6%; Pred. No. 9.5e-134;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQTWILTCIYQLLLFNPLVKTGICRRVTNNVQVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQTWILTCIYQLLLFNPLVKTGICRRVTNNVQVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPBHCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIYVDLVECKENSS 120
DB 61 MDVLPBHCWISSEWVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIYVDLVECKENSS 120
QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLIIGFAFGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLIIGFAFGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273

RESULT 11
US-09-224-681-48
Sequence 48, Application US/09224681

Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48

Query Match 99.6%; Score 1392; DB 3; Length 273;
Best Local Similarity 99.6%; Pred. No. 9.5e-134;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYIQLLFPNPLVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKYVG 60
DB 1 MKKTQWILTCIYIQLLFPNPLVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECKVENS 120

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DB 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECKVENS 120
QY 121 KOLKSFSPSPRLTPTPEFPRIENRSDAFDPVASETSCVVSSTLSPKDSRVST 180
DB 121 KOLKSFSPSPRLTPTPEFPRIENRSDAFDPVASETSCVVSSTLSPKDSRVST 180
QY 181 KPFMLPVAASLRNDSSSNRKNKPNPGDSSLHMAALPALFSLIIGFAGALYMKR 240
DB 181 KPFMLPVAASLRNDSSSNRKNKPNPGDSSLHMAALPALFSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLQEKREPFQEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKREPFQEV 273

RESULT 12
US-08-482-918-50
Sequence 50, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-50

Query Match 98.9%; Score 1381; DB 3; Length 273;
Best Local Similarity 98.9%; Pred. No. 1.3e-132;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYIQLLFPNPLVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKYVG 60
DB 1 MKKTQWILTCIYIQLLFPNPLVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECKVENS 120
DB 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECKVENS 120
QY 121 KOLKSFSPSPRLTPTPEFPRIENRSDAFDPVASETSCVVSSTLSPKDSRVST 180

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Db 121 KDLKKSFKSPERLFTPEEFRIFNRSIDAFKDFAVASSETDCVVSSTLSPEKDSRVST 180
Qy 181 KPFLPVAASSLRNSSSSNRKAKNPBGSSLHWAAMLPALFSLIIGFAGALYMKR 240
Db 181 KPFLPVAASSLRNSSSSNRKAKNPBGSSLHWAAMLPALFSLIIGFAGALYMKR 240
Qy 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 13
US-09-224-681-50
Sequence 50, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-50

Query Match 98.9%; Score 1381; DB 3; Length 273;
Best Local Similarity 98.9%; Pred. No. 1.3e-133;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKKTQWILFCIYQLLFPNPLVKTGICRRNVTNNVQVTKLVANLPKDYMTLKYPVG 60
Db 1 MKKTQWILFCIYQLLFPNPLVKTGICRRNVTNNVQVTKLVANLPKDYMTLKYPVG 60
Qy 61 MDVLPSCWISWMVQVSDSLTDLLDKFSNISEGINSYIIDKLVNIYDVLVECKENSS 120
Db 61 MDVLPSCWISWMVQVSDSLTDLLDKFSNISEGINSYIIDKLVNIYDVLVECKENSS 120
Qy 121 KDLKKSFKSPERLFTPEEFRIFNRSIDAFKDFAVASSETDCVVSSTLSPEKDSRVST 180
Db 121 KDLKKSFKSPERLFTPEEFRIFNRSIDAFKDFAVASSETDCVVSSTLSPEKDSRVST 180
Qy 181 KPFLPVAASSLRNSSSSNRKAKNPBGSSLHWAAMLPALFSLIIGFAGALYMKR 240
Db 181 KPFLPVAASSLRNSSSSNRKAKNPBGSSLHWAAMLPALFSLIIGFAGALYMKR 240
Qy 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 14
US-08-336-728A-50
Sequence 50, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-36-728A-50

Query Match 98.6%; Score 1378; DB 3; Length 273;
Best Local Similarity 98.5%; Pred. No. 2,5e-132;
Matches 269; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYQLLLFNPLVTEGICRNFVNNVQVTKLVANLPKQWITLKYYVG 60
DB 1 MKKTQWITLCIYQLLLFNPLVTEGICRNFVNNVQVTKLVANLPKQWITLKYYVG 60
QY 61 MDVLSHCISMVWVQVLSLTDLLDKFENISEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLSHCISMVWVQVLSLTDLLDKFENISEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KOLKSFSPERLFTPEEFRIIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVST 180
DB 121 KOLKSFSPERLFTPEEFRIIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVST 180
QY 181 KPFMLPVVASSLRNDSSSNRKAQNPQDSSLHMAAMLPALFSLIIGFAGALYWKRR 240
DB 181 KPFMLPVVASSLRNDSSSNRKAQNPQDSSLHMAAMLPALFSLIIGFAGALYWKRR 240
QY 241 QPSLTRAVENTIOINEDNEISMLQEKERFQEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLQEKERFQEV 273

RESULT 15
US-08-955-848A-82
Sequence 82, Application US/08955848A
Patent No. 5969105
GENERAL INFORMATION:
APPLICANT: Mc Whorter, Charles
TITLE OF INVENTION: No. 5969105el Stem Cell Factor Receptor
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: G. D. Searle & Co.
STREET: P. O. Box 5110
CITY: Chicago
STATE: IL
COUNTRY: U. S. A.
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,848A
FILING DATE: 21-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,165
FILING DATE: 25-OCT-1997
ATTORNEY/AGENT INFORMATION:

NAME: Bennett, Dennis A
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2992/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-737-6986
TELEFAX: 314-737-6972
TELEX:
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-955-848A-82

Query Match 90.6%; Score 1265; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 7.1e-121;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EGICRNRVTNNVQVTKLVANLPKQWITLKYYVQMDVLPSCWISSEWVQVLSLTDLL 85
DB 1 EGICRNRVTNNVQVTKLVANLPKQWITLKYYVQMDVLPSCWISSEWVQVLSLTDLL 85
QY 86 DKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS KD LKSFSPERLFTPEEFRIEN 145
DB 61 DKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS KD LKSFSPERLFTPEEFRIEN 120
QY 146 RSIDAFKDFVASETSDCVSSTLSPKDSRVSTKPFMLPVVASSLRNDSSSNRKAQ 205
DB 121 RSIDAFKDFVASETSDCVSSTLSPKDSRVSTKPFMLPVVASSLRNDSSSNRKAQ 180
QY 206 NPPGDSLHMAAMLPALFSLIIGFAGALYWKRRQPSLTRAVENTIOINEDNEISMLQ 265
DB 181 NPPGDSLHMAAMLPALFSLIIGFAGALYWKRRQPSLTRAVENTIOINEDNEISMLQ 240
QY 266 KEREFQEV 273
DB 241 KEREFQEV 248

Search completed: February 5, 2004, 15:12:23
Job time : 15.2893 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:07:35 ; Search time 30.4587 Seconds
(without alignments)
1876.686 Million cell updates/sec

Title: US-09-224-683-61

Perfect score: 1397
Sequence: 1 MKKTQWILITCIYQLLLEN.....NEEDNEISMLQEKERFQEV 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications_AA*

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2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1397	100.0	273	9	US-09-005-243-49
2	1397	100.0	273	9	US-09-005-243-61
3	1397	100.0	273	9	US-09-224-683-49
4	1397	100.0	273	9	US-09-224-683-61
5	1392	99.6	273	9	US-09-005-243-48
6	1392	99.6	273	9	US-09-224-683-48
7	1381	98.9	273	9	US-09-005-243-50
8	1381	98.9	273	9	US-09-224-683-50
9	1332.5	88.2	266	9	US-09-005-243-57
10	1332.5	88.2	266	9	US-09-224-683-57
11	1231	88.1	245	9	US-09-005-243-63
12	1231	88.1	245	9	US-09-224-683-63
13	1180.5	84.5	274	9	US-09-005-243-51
14	1180.5	84.5	274	9	US-09-224-683-51
15	1179.5	84.4	271	9	US-09-005-243-52

16	1179.5	84.4	271	9	US-09-224-683-52
17	1173	84.0	273	9	US-09-005-243-53
18	1173	84.0	273	9	US-09-224-683-53
19	1158	82.9	273	9	US-09-005-243-42
20	1158	82.9	273	9	US-09-224-683-42
21	1157	82.8	273	9	US-09-005-243-55
22	1157	82.8	273	9	US-09-224-683-55
23	1157	82.8	273	15	US-10-132-245-4
24	1151	82.4	273	9	US-09-005-243-54
25	1151	82.4	273	9	US-09-224-683-54
26	1066	76.3	270	15	US-10-132-245-2
27	1030	73.7	208	9	US-09-005-243-42
28	1030	73.7	208	9	US-09-224-683-46
29	865	61.9	195	9	US-09-005-243-44
30	865	61.9	195	9	US-09-224-683-44
31	843	60.3	166	9	US-09-748-592-2
32	839	60.1	164	10	US-09-903-327A-10
33	839	60.1	165	12	US-10-320-231A-25
34	839	60.1	165	15	US-10-053-355A-2
35	839	60.1	393	15	US-10-270-555-1
36	837	59.9	613	10	US-09-903-327A-14
37	826	59.1	196	9	US-09-005-243-40
38	826	59.1	196	9	US-09-224-683-40
39	683	48.9	282	9	US-09-005-243-56
40	683	48.9	282	9	US-09-224-683-56
41	679	48.6	165	9	US-09-005-243-1
42	679	48.6	165	9	US-09-224-683-1
43	667	47.7	393	15	US-10-270-555-2
44	315	22.5	82	9	US-09-005-243-59
45	315	22.5	82	9	US-09-224-683-59

ALIGNMENTS

RESULT 1
US-09-005-243-49
; Sequence 49, Application US/09005243
; Patent No. US20020018763A1
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,243
; FILING DATE:
; CLASSIFICATION:
; APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-49

Query Match 100.0%; Score 1397; DB 9; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMTTLKVP 60
DB 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMTTLKVP 60
QY 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIVDLVECKENSS 120
DB 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIVDLVECKENSS 120
QY 121 KDLKSKFSPPEPRLFTPEEFRIFNRSIDAFKDFVAVASETSDCVSSSTLSPEKDSRVSVT 180
DB 121 KDLKSKFSPPEPRLFTPEEFRIFNRSIDAFKDFVAVASETSDCVSSSTLSPEKDSRVSVT 180
QY 181 KPEMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAALPALPSLIIGFAGALYMKR 240
DB 181 KPEMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAALPALPSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 2

US-09-005-243-61
Sequence 61, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-61

Query Match 100.0%; Score 1397; DB 9; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMTTLKVP 60
DB 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMTTLKVP 60
QY 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIVDLVECKENSS 120
DB 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIVDLVECKENSS 120
QY 121 KDLKSKFSPPEPRLFTPEEFRIFNRSIDAFKDFVAVASETSDCVSSSTLSPEKDSRVSVT 180
DB 121 KDLKSKFSPPEPRLFTPEEFRIFNRSIDAFKDFVAVASETSDCVSSSTLSPEKDSRVSVT 180
QY 181 KPEMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAALPALPSLIIGFAGALYMKR 240
DB 181 KPEMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAALPALPSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 3

US-09-224-683-49
Sequence 49, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-49

Query Match 100.0%; Score 1397; DB 9; Length 273;
Best Local Similarity 100.0%; Pred. No. 1,8e-127;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICNRRTNNKDYTKYVANI PKRYMTTLKYPG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICNRRTNNKDYTKYVANI PKRYMTTLKYPG 60
QY 61 MDVLPSCWISSEMYVSDSLTDLDKFSNISSEGLSYSTIIDKLVNIVDDLVCVENNS 120
DB 61 MDVLPSCWISSEMYVSDSLTDLDKFSNISSEGLSYSTIIDKLVNIVDDLVCVENNS 120
QY 121 KDLSKFSKSPRLFTPEEFRRIFNRSIDAFKDFVVAESVSDCVSSSTLSPKDSRVSVT 180
DB 121 KDLSKFSKSPRLFTPEEFRRIFNRSIDAFKDFVVAESVSDCVSSSTLSPKDSRVSVT 180

QY 181 KPMLPVAASLRNDSSSNRKAKNPPGDSLLHMAALPALPSLLIGFAGALYWKX 240
DB 181 KPMLPVAASLRNDSSSNRKAKNPPGDSLLHMAALPALPSLLIGFAGALYWKX 240
QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREPOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREPOEV 273

RESULT 4
US-09-224-683-61
Sequence 61, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 100.0%; Score 1397; DB 9; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFPNPLVKTGICNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWTLTCTIYQLLFPNPLVKTGICNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISGLSNYSIIDKLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISGLSNYSIIDKLVNIYDDLVCEKENS 120
QY 121 KDLKKSFKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKKSFKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSNRKAQNPQDSSLHMAALPALFSLIIGFAGALYMKR 240
DB 181 KPFLPVAASSLRNDSSSNRKAQNPQDSSLHMAALPALFSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273

RESULT 5

US-09-005-243-48
Sequence 48, Application US/09005243
Patent No. US20020018763A1

GENERAL INFORMATION:

APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseleman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-0448
TELEFAX: 312/474-6300
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 99.6%; Score 1392; DB 9; Length 273;
Best Local Similarity 99.6%; Pred. No. 5.6e-127;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFPNPLVKTGICNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWTLTCTIYQLLFPNPLVKTGICNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISGLSNYSIIDKLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISGLSNYSIIDKLVNIYDDLVCEKENS 120
QY 121 KDLKKSFKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKKSFKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSNRKAQNPQDSSLHMAALPALFSLIIGFAGALYMKR 240
DB 181 KPFLPVAASSLRNDSSSNRKAQNPQDSSLHMAALPALFSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273

RESULT 6

US-09-224-683-48
Sequence 48, Application US/09224683
Patent No. US2002001491A1

GENERAL INFORMATION:

APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseleman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-48

Query Match 99.6%; Score 1392; DB 9; Length 273;
Best Local Similarity 99.6%; Pred. No. 5.6e-127;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWMLTCTIYQLLFPNPLVKTGICRNRTNNVQDTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWMLTCTIYQLLFPNPLVKTGICRNRTNNVQDTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDLKSKFSKPEPRLPFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 180
DB 121 KDLKSKFSKPEPRLPFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 180
QY 181 KPFMLPVAASSLRNDSSSNRKAQNPQDSSLHMAAMLPALFSLITGFAFALYWKRR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAQNPQDSSLHMAAMLPALFSLITGFAFALYWKRR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273

RESULT 7
US-09-005-243-50
Sequence 50, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Boseelman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-50

Query Match 98.9%; Score 1381; DB 9; Length 273;
Best Local Similarity 98.9%; Pred. No. 6.5e-126;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWMLTCTIYQLLFPNPLVKTGICRNRTNNVQDTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWMLTCTIYQLLFPNPLVKTGICRNRTNNVQDTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDLKSKFSKPEPRLPFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 180
DB 121 KDLKSKFSKPEPRLPFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 180
QY 181 KPFMLPVAASSLRNDSSSNRKAQNPQDSSLHMAAMLPALFSLITGFAFALYWKRR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAQNPQDSSLHMAAMLPALFSLITGFAFALYWKRR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273

RESULT 8

US-09-224-683-50
Sequence 50, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-50

Query Match 98.9%; Score 1381; DB 9; Length 273;
Best Local Similarity 98.9%; Pred. No. 6.5e-126;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRRNVTNNVADVTQLVANLPRDYMILTKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRRNVTNNVADVTQLVANLPRDYMILTKYVPG 60
QY 61 MDVLPSCWISMMVQVLSLTDLLDKFSNISEGISNYSIIDKLVNIYDDLVECKENSS 120
DB 61 MDVLPSCWISMMVQVLSLTDLLDKFSNISEGISNYSIIDKLVNIYDDLVECKENSS 120
QY 121 KOLKSFSPERPLTPPEFPFRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVSVT 180
DB 121 KOLKSFSPERPLTPPEFPFRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVSVT 180
QY 181 KFMPLPVAASSLRNDSSSNRKAKNPPGDSGLHWAAMALPALFSLIIGFAFALYMKR 240
DB 181 KFMPLPVAASSLRNDSSSNRKAKNPPGDSGLHWAAMALPALFSLIIGFAFALYMKR 240
QY 241 QPSLTRAVENTIOINEEDNEISMLQKEKEFEQEV 273
DB 241 QPSLTRAVENTIOINEEDNEISMLQKEKEFEQEV 273

RESULT 9

US-09-005-243-57
Sequence 57, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-57

Query Match 88.2%; Score 1232.5; DB 9; Length 266;
Best Local Similarity 91.9%; Pred. No. 1.7e-111;
Matches 251; Conservative 9; Mismatches 6; Indels 7; Gaps 5;

QY 1 MKKTQWMLITCIYQLLHFNPLVKEGICRNRVTNNVKDVTXVANI.PKDYMITLKYVG 60
DB 1 MKKTQWMLITCIYQLLHFNPLVKT-GICRNRVT-DVKDVTXVANI.PKDYMITLKYVG 58
QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVINVDLVECVENSS 120
DB 59 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVIQVDDLVLC-ENSS 117
QY 121 KDLKSKFSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 180
DB 118 KKVKS-KSPEPLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 176
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPGDSSLHMAAMLPALFSLIIGFAGALYWKRR 240
DB 177 KPFMLPVAASSLRNDSSSNRKANE---DSSLQMAAMLPALFSLVIGFAGALYWKRR 233
QY 241 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 273
DB 234 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 266

RESULT 10

US-09-224-683-57
Sequence 57, Application US/09224683
Patent No. US2002003191A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Boeselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255

FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-57

Query Match 88.2%; Score 1232.5; DB 9; Length 266;
Best Local Similarity 91.9%; Pred. No. 1.7e-111;
Matches 251; Conservative 9; Mismatches 6; Indels 7; Gaps 5;

QY 1 MKKTQWMLITCIYQLLHFNPLVKEGICRNRVTNNVKDVTXVANI.PKDYMITLKYVG 60
DB 1 MKKTQWMLITCIYQLLHFNPLVKT-GICRNRVT-DVKDVTXVANI.PKDYMITLKYVG 58
QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVINVDLVECVENSS 120
DB 59 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVIQVDDLVLC-ENSS 117
QY 121 KDLKSKFSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 180
DB 118 KKVKS-KSPEPLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPKDSRVST 176
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPGDSSLHMAAMLPALFSLIIGFAGALYWKRR 240
DB 177 KPFMLPVAASSLRNDSSSNRKANE---DSSLQMAAMLPALFSLVIGFAGALYWKRR 233
QY 241 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 273
DB 234 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 266

RESULT 11

US-09-005-243-63
Sequence 63, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Boeselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-63

Query Match 88.1%; Score 1231; DB 9; Length 245;
Best Local Similarity 89.4%; Pred. No. 2.2e-111;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQTWILTCIYQLLEFNPVLTKEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQTWILTCIYQLLEFNPVLTKEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSENVVQSLDITLDDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
DB 61 MDVLPSCWISSENVVQSLDITLDDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
QY 121 KDLKSKFKSPPPLFTPEEFRIENRSIDAFKDFVAVASTSPCVVSTISPEKDSVSVT 180
DB 121 KDLKSKFKSPPPLFTPEEFRIENRSIDAFKDFVAVASTSPCVVSTISPEKDSVSVT 180
QY 121 KDLKSKFKSPPPLFTPEEFRIENRSIDAFKDFVAVASTSPCVVSTISPEKDSVSVT 174
DB 121 KDLKSKFKSPPPLFTPEEFRIENRSIDAFKDFVAVASTSPCVVSTISPEKDSVSVT 174
QY 181 KEFMLPVAASLRNDSSSNRKAKNPQGDSSILHMAAALPALFSLIIFAFGALYWKKR 240
DB 175 -----KAKNPQGDSSILHMAAALPALFSLIIFAFGALYWKKR 212
QY 241 QPSLTPAVENIQINEEDNEISMLOEKERPEOEY 273
DB 213 QPSLTPAVENIQINEEDNEISMLOEKERPEOEY 245

RESULT 12
US-09-224-683-63
Sequence 63, Application US/09224683
Patent No. US20020031491A1

GENERAL INFORMATION:
APPLICANT: Zeebo, Kriesztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-63

Query Match 88.1%; Score 1231; DB 9; Length 245;
Best Local Similarity 89.4%; Pred. No. 2.2e-111;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQTWILTCIYQLLEFNPVLTKEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQTWILTCIYQLLEFNPVLTKEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSENVVQSLDITLDDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
DB 61 MDVLPSCWISSENVVQSLDITLDDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120

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0Y      121  KDLKSKSKSEPRFLTFEEEFRRFJFNSIDAFKDFVASTSDCVVSTLSEKXSRVSVT 180
0Y      121  KDLKSKSKSEPRFLTFEEEFRRFJFNSIDAFKDFVASTSDCVVSTLSEKXSRVSVT 180
Db      121  KDLKSKSKSEPRFLTFEEEFRRFJFNSIDAFKDFVASTSDCVVSTLSEKXSRVSVT 180
0Y      181  KPFLMPEVAASSLRNDSSSNRRKAKNP PGDSSLIHMAAVALPALFSLIIGFAGALYWKKR 240
Db      175  -----KAKNP PGDSSLIHMAAVALPALFSLIIGFAGALYWKKR 2212
0Y      241  QPSLITRAVENIQINEEDNEISMLQERERFQEV 273
Db      213  QPSLITRAVENIQINEEDNEISMLQERERFQEV 245

RESULT 13
US-09-005-243-51
Sequence 51, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: single

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;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-09-005-243-51

Query Match          84.5%; Score 1180.5; DB 9; Length 274;
Best Local Similarity 85.4%; Pred. No. 2.1e-106;
Matches 234; Conservative 17; Mismatches 22; Indels 1; Gaps 1

QY      1 MKKTQWILTCIYLQLLFLNPLVTKEGICRRRVNNVDYTKLVANIPKDTMTLKVPVG 60
       1 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      1 MKKTQWIIITCIYLLQLLFNPLVKTKGICGRVYDDVDYTKLVANIPKDYKIALKVPG 60
       1 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      61 MDVLPSHCISEWVQVOLDSDLTDLDKFSNI SEGLSNYSIIDKLWNIVDDLVECVKENSS 120
       61 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      61 MDVLPSHCHISWVEQLSVSLTDLDDKSNISIEGLSNYSIIDKLWKYVDLVECTBSYSF 120
       61 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      121 KDLKSFKSPPEPLFTPEEFERIFNRSIDAKDF-VVASETSDCVSSTLSPEKDSRSVY 179
       121 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      121 ENVKAKPKPELRFLTPEEFPRIFNRSIDAFKDELTAVSXSECVSSTLSPDKDSRSVY 180
       121 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      180 TKFPMLPVVAASGLRNDSSSNRKAKNPQGSSLHMAAMALPALFSIIGPAGALYMKK 239
       180 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      181 TKFPMLPVVAASGLRNDSSSNRKASNSIGSNSIQMAMALPAFFSVIGPAGALYMKK 240
       181 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      240 RQSLTRAVENIOINEENESIMLOEKREPOEV 273
       240 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      241 KQNLTRIVENIOINEENESIMLOEKEREFOEV 274
       241 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 14
US-09-224-683-51
; Sequence 51, Application US/09224683
; Patent No. US20020031491A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor: Composition Claims
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,683
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990

```

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-51

Query Match      84.5%; Score 1180.5; DB 9; Length 274;
Best Local Similarity 85.4%; Pred. No. 2.1e-106;
Matches 234; Conservative 17; Mismatches 22; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPVLVKTGICNRVTNNVKDVKLVANLPKDYMTLLKVVVG 60
DB 1 MKKTQWILTCIYLQLLFNPVLVKTGICNRVTNNVKDVKLVANLPKDYMTLLKVVVG 60
QY 61 MDVLPSCWISWVVOVLSLTDLDKFSNISSEGLSNYSIIDLVNIIVDDVLCVCKENS 120
DB 61 MDVLPSCWISWVVOVLSLTDLDKFSNISSEGLSNYSIIDLVNIIVDDVLCVCKENS 120
QY 61 MDVLPSCWISWVVOVLSLTDLDKFSNISSEGLSNYSIIDLVNIIVDDVLCVCKENS 120
DB 61 MDVLPSCWISWVVOVLSLTDLDKFSNISSEGLSNYSIIDLVNIIVDDVLCVCKENS 120
QY 121 KDIKSKFSPDEPLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKDSRVSV 179
DB 121 ENVKKAPKSPBELFTPEEFRIFNRSIDAFKDFTVASGSCVVSSTLSPKDSRVSV 180
QY 180 TPEFMLPVAASSLRNDSSSNRKAKNPQDSSIHMAAMALPALFSLIIGFAFGALYWK 239
DB 181 TPEFMLPVAASSLRNDSSSNRKASNSIGDSMLQAAVALPAPFSLVIGFAGALYWK 240
QY 240 RPSLTRAVENTIOINEEDNEISMLOEKEREFQEV 273
DB 241 KQPNLTRVTENIOINEEDNEISMLOEKEREFQEV 274

RESULT 15
US-09-005-243-52
Sequence 52, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristzina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
```

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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-52

Query Match      84.4%; Score 1179.5; DB 9; Length 271;
Best Local Similarity 86.4%; Pred. No. 2.5e-106;
Matches 235; Conservative 17; Mismatches 17; Indels 3; Gaps 3;

QY 3 KTQWILTCIYLQLLFNPVLVKTGICNRVTNNVKDVKLVANLPKDYMTLLKVVPM 62
DB 2 KTQWILTCIYLQLLFNPVLVKTGICNRVTNNVKDVKLVANLPKDYMTLLKVVPM 60
QY 63 VLPSCWISWVVOVLSLTDLDKFSNISSEGLSNYSIIDLVNIIVDDVLCVCKENS 122
DB 61 VLPSCWISWVVOVLSLTDLDKFSNISSEGLSNYSIIDLVNIIVDDVLCVCKENS 120
QY 123 LKSKFSPDEPLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKDSRVSV 181
DB 121 VKSKSPDEPLFTPEEFRIFNRSIDAFKDFVAVASSTLSPKDSRVSV 180
QY 182 PFMPLPVAASSLRNDSSSNRKAKNPQDSSIHMAAMALPALFSLIIGFAFGALYWK 241
DB 181 PFMPLPVAASSLRNDSSSNRKAT-NPIEDSSIQAAVALPAPFSLVIGFAGALYWK 239
QY 242 PSLTRAVENTIOINEEDNEISMLOEKEREFQEV 273
DB 240 PNLTRVTENIOINEEDNEISMLOEKEREFQEV 271
```

Search completed: February 5, 2004, 15:23:27
Job time : 31.4587 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:00:43 ; Search time 15.4174 Seconds
(without alignments)
1702.889 Million cell updates/sec

Title: US-09-224-683-61

Perfect score: 1397
Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISMLQEKERFQEV 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1397	100.0	273	2	A35974	mast cell growth f
2	1231	88.1	245	2	B61190	mast cell growth f
3	1203.5	86.1	274	2	I46575	c-kit ligand - pig
4	1184.5	84.8	274	2	S47571	stem cell factor,
5	1180.5	84.5	274	2	I46929	stem cell factor -
6	1157	82.8	273	2	S65801	mast cell growth f
7	991	70.9	245	2	A37934	mast cell growth f
8	885.5	63.4	202	2	S58313	stem cell factor p
9	857	60.3	201	2	B35974	stem cell factor p
10	703	50.3	287	2	JN0637	stem cell factor p
11	702	50.3	287	2	S70366	stem cell factor 1
12	589	42.2	253	2	S70367	stem cell factor 1
13	576.5	41.3	124	2	S29052	stem cell factor s
14	175.5	12.6	51	2	B35971	mast cell growth f
15	172.5	12.3	49	2	A35971	mast cell growth f
16	106	7.6	465	2	H97165	flagellar hook-len
17	101	7.2	1490	2	T16086	hypothetical prote
18	100.5	7.2	402	2	T09062	probable advanced
19	100.5	7.2	647	2	F90585	conserved hypothet
20	97.5	7.0	1107	2	S61667	probable membrane
21	97	6.9	1447	2	F82909	hypothetical prote
22	95.5	6.8	484	2	T25944	hypothetical prote
23	95.5	6.7	1293	2	B86461	probable protein k
24	93.5	6.7	1293	2	T27886	hypothetical prote
25	93.5	6.7	1813	2	T19295	hypothetical prote
26	92.5	6.6	164	2	B69616	cell-division init
27	92.5	6.6	246	2	T19850	hypothetical prote
28	92.5	6.6	398	2	I53340	paired box transcr
29	92.5	6.6	512	2	G86773	citrate (pro-3s)-1

30	91.5	6.5	575	2	D84668	hypothetical prote
31	91.5	6.5	767	2	T19690	hypothetical prote
32	90.5	6.5	251	2	B86647	hypothetical prote
33	90.5	6.5	616	2	A69136	ATP-dependent Clp
34	90.5	6.5	1425	2	E89303	protein C47E8.8 fi
35	90.5	6.5	1675	2	T31473	hypothetical prote
36	90	6.4	378	2	F64300	formate dehydrogen
37	90	6.4	774	2	T32987	formate dehydrogen
38	90	6.4	2100	2	T38128	c7123.15 protein -
39	89.5	6.4	268	2	G81257	probable hemetin up
40	89.5	6.4	335	2	S44922	K18 antigen - Entra
41	89.5	6.4	384	2	H64161	hypothetical prote
42	89	6.4	242	2	T27226	hypothetical prote
43	89	6.4	292	2	B71733	hypothetical prote
44	89	6.4	982	2	T15967	hypothetical prote
45	88.5	6.3	378	2	T25672	hypothetical prote

ALIGNMENTS

RESULT 1

A35974
mast cell growth factor precursor - human
N:Alternate names: Kit ligand; stem cell factor
C:Species: Homo sapiens (man)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C/Accession: A35974; A61190
S:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.J.
S; J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, I
Cell 63, 203-211, 1990
A>Title: Primary structure and functional expression of rat and human stem cell factor 1
A:Reference number: A35974; MUID:91004219; PMID:12208279
A:Accession: A35974
A:Molecule type: mRNA
A:Residues: 1-273 <MAR>
A:Cross-references: GB:M59964; NID:G37933; PIDN:AAA85450.1; PID:G37934
R:Anderson, D.M.; Williams, D.E.; Tushnets, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, J
Cell Growth Differ. 2, 373-378, 1991
A>Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiz
A:Reference number: A61190; MUID:92172791; PMID:1724381
A:Accession: A61190
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-273 <AND>
C:Genetics: GDB:MGF
A:Gene: GDB:MGF
A:Cross-references: GDB:128026; OMIM:184745
A:Map position: 12q22-12q22
C:Superfamily: mouse mast cell growth factor
C:Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane pro
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-273/Product: mast cell growth factor #status predicted <MCS>
F;26-189/Product: (or 26-190) mast cell growth factor, soluble form #status predicted <I
F;215-237/Domain: transmembrane #status predicted <TM>
F;90,97,118,145,195/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 1397; DB 2; Length 273;

Best Local Similarity 100.0%; Pred. No. 6.6e-103;

Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNVQVTLVNLKPDVMTTLKYVPG	60
DB	1	MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNVQVTLVNLKPDVMTTLKYVPG	60
QY	61	MDVLSHCWISSEMVQSLTDLDDKFSNISSEGLSNYSIIDKLVINIYVDLVECVKENS	120
DB	61	MDVLSHCWISSEMVQSLTDLDDKFSNISSEGLSNYSIIDKLVINIYVDLVECVKENS	120
QY	121	KDLKSFSPPEPRLLTPPEEFRIFNRSIDAFKDPVVAASSTSCVVSSTLSPKDSRVST	180
DB	121	KDLKSFSPPEPRLLTPPEEFRIFNRSIDAFKDPVVAASSTSCVVSSTLSPKDSRVST	180

QY 181 KPMPLPVAAASLRNDSSSNRKAQPPGSSSLHMAAMALPALFSLIIGFAGALYWKRR 240
 Db 181 KPMPLPVAAASLRNDSSSNRKAQPPGSSSLHMAAMALPALFSLIIGFAGALYWKRR 240
 QY 241 QPSTRAVENIQINEEDNEISMLQEKEREFQEV 273
 Db 241 QPSTRAVENIQINEEDNEISMLQEKEREFQEV 273

RESULT 2

B61190
 mast cell growth factor, short form precursor - human
 N:Alternate names: Kit ligand, short form; stem cell factor, short form
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence_rev: 03-May-1994 #text_change 21-Jul-2000
 C:Accession: B61190
 R:Anderson, D.M.; Williams, D.E.; Teshinski, R.; Gimpel, S.; Eisenman, J.; Camnizzaro, L.
 Cell Growth Differ. 2, 373-378, 1991
 A:Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiza
 A:Reference number: A61190; MUID:92172791; PMID:1724381
 A:Accession: B61190
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-245 <AND>
 C:Comment: Alternative splicing produces this short form in which a predicted cleavage s
 C:Gene: GDB:MGF
 A:Cross-references: GDB:128026; OMIM:184745
 A:Map position: 12q22-12q22
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: alternative splicing; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:187-209/Domain: transmembrane #status predicted <TMN>
 F:90,97,118,145/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.1%; Score 1231; DB 2; Length 245;
 Best Local Similarity 89.4%; Pred. No. 7, 3e-90;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWTLITCTYQLLFNPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYYVG 60
 Db 1 MKKTQWTLITCTYQLLFNPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYYVG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVNIIVDVLVECVKENS 120
 Db 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVNIIVDVLVECVKENS 120
 QY 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 180
 Db 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 180
 QY 181 KPMPLPVAAASLRNDSSSNRKAQPPGSSSLHMAAMALPALFSLIIGFAGALYWKRR 240
 Db 181 KPMPLPVAAASLRNDSSSNRKAQPPGSSSLHMAAMALPALFSLIIGFAGALYWKRR 240
 QY 241 QPSTRAVENIQINEEDNEISMLQEKEREFQEV 273
 Db 241 QPSTRAVENIQINEEDNEISMLQEKEREFQEV 273

RESULT 3

146575
 c-kit ligand - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_rev: 21-Feb-1997 #text_change 21-Jul-2000
 C:Accession: I46575
 R:Zhang, Z.; Anthony, R.V.
 Biol. Reprod. 50, 95-102, 1994
 A:Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization
 A:Reference number: I46575; MUID:94146218; PMID:7508758
 A:Accession: I46575
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-274 <ZHA>
 A:Cross-references: GB:I07786; NID:9164420; PIDN:AAA53670.1; PID:9164421
 C:Superfamily: mouse mast cell growth factor

Query Match 86.1%; Score 1203.5; DB 2; Length 274;
 Best Local Similarity 85.8%; Pred. No. 1, 3e-87;
 Matches 235; Conservative 22; Mismatches 16; Indels 1; Gaps 1;

QY 1 MKKTQWTLITCTYQLLFNPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYYVG 60
 Db 1 MKKTQWTLITCTYQLLFNPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYYVG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVNIIVDVLVECVKENS 120
 Db 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVNIIVDVLVECVKENS 120
 QY 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 179
 Db 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 180
 QY 181 KPMPLPVAAASLRNDSSSNRKAQPPGSSSLHMAAMALPALFSLIIGFAGALYWKRR 239
 Db 181 KPMPLPVAAASLRNDSSSNRKAQPPGSSSLHMAAMALPALFSLIIGFAGALYWKRR 240
 QY 240 ROPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
 Db 241 ROPSLTRAVENIQINEEDNEISMLQEKEREFQEV 274

RESULT 4

S47571
 stem cell factor, longer isoform - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 27-Jan-1995 #sequence_rev: 27-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S47571
 R:Zhou, J.H.; Htkono, H.; Ohnaki, M.; Kubota, T.; Sakurai, M.
 Biochim. Biophys. Acta 1223, 148-150, 1994
 A:Title: Cloning and characterization of cDNAs encoding two normal isoforms of bovine st
 A:Reference number: S47571; MUID:94339176; PMID:7520283
 A:Accession: S47571
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-274 <ZHO>
 A:Cross-references: EMBL:D28934; NID:9538520; PIDN:BA06061.1; PID:9538521
 C:Superfamily: mouse mast cell growth factor

Query Match 84.8%; Score 1184.5; DB 2; Length 274;
 Best Local Similarity 84.7%; Pred. No. 4e-86;
 Matches 232; Conservative 20; Mismatches 21; Indels 1; Gaps 1;

QY 1 MKKTQWTLITCTYQLLFNPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYYVG 60
 Db 1 MKKTQWTLITCTYQLLFNPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYYVG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVNIIVDVLVECVKENS 120
 Db 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVNIIVDVLVECVKENS 120
 QY 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 179
 Db 121 KDLKSKFSPPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 180
 QY 180 TKPFLPVAASSLRNDSSSNRKAQPPGSSSLHMAAMALPALFSLIIGFAGALYWKRR 239
 Db 181 TKPFLPVAASSLRNDSSSNRKAQPPGSSSLHMAAMALPALFSLIIGFAGALYWKRR 240
 QY 240 ROPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
 Db 241 ROPSLTRAVENIQINEEDNEISMLQEKEREFQEV 274

RESULT 5

I46929

QY 241 QPSLTRAVENTIQINEEDNEISMLQEKERFEQEV 273
 Db 241 QSSLTRAVENIQINEEDNEISMLQEKERFEQEV 273

RESULT 7

Query Match 70.9%; Score 991; DB 2; Length 245;
 Best Local Similarity 72.2%; Pred. No. 6.5e-71;
 Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;
 A:Accession: A37934
 A:Molecule type: mRNA
 A:Residues: 1-245 <FLA>
 A:Cross-references: GB:M64262
 R/Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992
 A>Title: Differential expression and processing of two cell associated forms of the kit-
 A:Reference number: A43751; MUID:92330001; PMID:1378327
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-173, 'R', 175-186, 'L', 188-245 <HUA>
 A:Cross-references: GB:S04534
 A:Note: the authors translated the codon TTG for residue 187 as Trp
 C:Superfamily: mouse mast cell growth factor

QY 1 MKKTQWTLITCIYQLLEFNPVKTGICRRNVTNNVKDVKLVANLPKDYMITLTKYVG 60
 Db 1 MKKTQWTLITCIYQLLEFNPVKTGICRRNVTNNVKDVKLVANLPKDYMITLTKYVG 60
 QY 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
 Db 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
 QY 121 KDLKSFSPSPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVASSTLSPEKDSRVSVT 180
 Db 121 KDLKSFSPSPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVASSTLSPEKDSRVSVT 180
 QY 121 KDLKSFSPSPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVASSTLSPEKDSRVSVT 180
 Db 121 KDLKSFSPSPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVASSTLSPEKDSRVSVT 180
 QY 181 KPFMLPVAASSLRNDSSSNRKANPPGDDSLHMAAMLPALFSLIGFAGALYMKR 240
 Db 181 KPFMLPVAASSLRNDSSSNRKANPPGDDSLHMAAMLPALFSLIGFAGALYMKR 240
 QY 175 -----KAKAPEDSGIQWTRMMLPLISLVIFAFGALYMKK 212
 Db 241 QPSLTRAVENTIQINEEDNEISMLQEKERFEQEV 273
 Db 213 QSSLTRAVENIQINEEDNEISMLQEKERFEQEV 245

RESULT 8

Query Match 63.4%; Score 885.5; DB 2; Length 202;
 Best Local Similarity 86.1%; Pred. No. 1.1e-62;
 Matches 174; Conservative 15; Mismatches 12; Indels 1; Gaps 1;
 A:Accession: A37934
 A:Molecule type: mRNA
 A:Residues: 1-245 <FLA>
 A:Cross-references: GB:M64262
 R/Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992
 A>Title: Differential expression and processing of two cell associated forms of the kit-
 A:Reference number: A43751; MUID:92330001; PMID:1378327
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-173, 'R', 175-186, 'L', 188-245 <HUA>
 A:Cross-references: GB:S04534
 A:Note: the authors translated the codon TTG for residue 187 as Trp
 C:Superfamily: mouse mast cell growth factor

Query Match 63.4%; Score 885.5; DB 2; Length 202;
 Best Local Similarity 86.1%; Pred. No. 1.1e-62;
 Matches 174; Conservative 15; Mismatches 12; Indels 1; Gaps 1;
 A:Accession: A37934
 A:Molecule type: mRNA
 A:Residues: 1-245 <FLA>
 A:Cross-references: GB:M64262
 R/Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992
 A>Title: Differential expression and processing of two cell associated forms of the kit-
 A:Reference number: A43751; MUID:92330001; PMID:1378327
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-173, 'R', 175-186, 'L', 188-245 <HUA>
 A:Cross-references: GB:S04534
 A:Note: the authors translated the codon TTG for residue 187 as Trp
 C:Superfamily: mouse mast cell growth factor

QY 1 MKKTQWTLITCIYQLLEFNPVKTGICRRNVTNNVKDVKLVANLPKDYMITLTKYVG 60
 Db 1 MKKTQWTLITCIYQLLEFNPVKTGICRRNVTNNVKDVKLVANLPKDYMITLTKYVG 60
 QY 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
 Db 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
 QY 121 KDLKSFSPSPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVASSTLSPEKDSRVSVT 179
 Db 121 KDLKSFSPSPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVASSTLSPEKDSRVSVT 180
 QY 180 TKPFMLPVAASSLRNDSSSN 201
 Db 181 TKPFMLPVAASSLRNDSSSN 202

RESULT 9

Query Match 61.3%; Score 857; DB 2; Length 201;
 Best Local Similarity 82.6%; Pred. No. 1.9e-60;
 Matches 166; Conservative 15; Mismatches 20; Indels 0; Gaps 0;
 A:Accession: B35974
 A:Molecule type: mRNA
 A:Residues: 1-201 <MAR>
 A:Cross-references: GB:M59966; NID:9206861; PIDN:AAA42117.1; PID:9554507
 R/Liu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zsebo, J.
 J. Biol. Chem. 266, 8102-8107, 1991
 A>Title: Amino acid sequence and post-translational modification of stem cell factor iso
 A:Reference number: A39805; MUID:91217037; PMID:1708771
 A:Accession: A39805
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-27-190 <LUA>
 C:Superfamily: mouse mast cell growth factor

QY 1 MKKTQWTLITCIYQLLEFNPVKTGICRRNVTNNVKDVKLVANLPKDYMITLTKYVG 60
 Db 1 MKKTQWTLITCIYQLLEFNPVKTGICRRNVTNNVKDVKLVANLPKDYMITLTKYVG 60
 QY 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
 Db 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
 QY 121 KDLKSFSPSPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVASSTLSPEKDSRVSVT 180
 Db 121 KDLKSFSPSPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVASSTLSPEKDSRVSVT 180
 QY 181 KPFMLPVAASSLRNDSSSN 201
 Db 181 KPFMLPVAASSLRNDSSSN 201

RESULT 10

Query Match 61.3%; Score 857; DB 2; Length 201;
 Best Local Similarity 82.6%; Pred. No. 1.9e-60;
 Matches 166; Conservative 15; Mismatches 20; Indels 0; Gaps 0;
 A:Accession: B35974
 A:Molecule type: mRNA
 A:Residues: 1-201 <MAR>
 A:Cross-references: GB:M59966; NID:9206861; PIDN:AAA42117.1; PID:9554507
 R/Liu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zsebo, J.
 J. Biol. Chem. 266, 8102-8107, 1991
 A>Title: Amino acid sequence and post-translational modification of stem cell factor iso
 A:Reference number: A39805; MUID:91217037; PMID:1708771
 A:Accession: A39805
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-27-190 <LUA>
 C:Superfamily: mouse mast cell growth factor

A:Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
C:Superfamily: mouse mast cell growth factor

Query Match 41.3%; Score 576.5; DB 2; Length 124;
Best Local Similarity 75.2%; Pred. No. 1.4e-38;
Matches 124; Conservative 0; Mismatches 0; Indels 41; Gaps 4;

QY 26 EGIQRNRVTNNVNDVKLVANLPKDYMITLKYPGMDVLPSCWISSEMYVQLSDSLTDL 85
DB 1 EGIQRNRVTNNVK-----DVLPSHCWISSEMYVQLS----- 30

QY 86 DKFSNISSEGLSNYSIIDKLNIIVDLVECVKENSXKDLKSKSPSPRLFTPEEFRI 145
DB 31 DKFSNISSEGLSNYSII-----DVLVECVKENSXKDLKSKSPSPRLFTPEEFRI 83

QY 146 RSLDAKDFVAVASSETSDCVVSSSTLSPKDSRVSVTKPFMLPPVAA 190
DB 84 RSI---DFVAVASSETSDCVVSSSTLSPKDSRVSVTKPFMLPPVAA 124

RESULT 14

B35971
mast cell growth factor - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: B35971

R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.
Cell 63, 167-174, 1990

A:Title: Identification of a ligand for the c-kit proto-oncogene.

A:Reference number: A35971; MUID:91004215; PMID:1698553

A:Accession: B35971

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-51 <WIL>

C:Superfamily: mouse mast cell growth factor

C:Keywords: transmembrane protein

Query Match 12.6%; Score 175.5; DB 2; Length 51;
Best Local Similarity 72.3%; Pred. No. 1.9e-07;
Matches 34; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 28 ICRNRVTNNVNDVKLVANLPKDYMITLKYPGMDVLPSCWISSEMY 74
DB 3 ICRNPVTNDVKITKLVANLPNDYMITLNVVAGMDVLP--WMLDDMI 48

RESULT 15

A35971
mast cell growth factor - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: A35971

R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.
Cell 63, 167-174, 1990

A:Title: Identification of a ligand for the c-kit proto-oncogene.

A:Reference number: A35971; MUID:91004215; PMID:1698553

A:Accession: A35971

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-49 <WIL>

C:Superfamily: mouse mast cell growth factor

C:Keywords: transmembrane protein

Query Match 12.3%; Score 172.5; DB 2; Length 49;
Best Local Similarity 73.5%; Pred. No. 3e-07;
Matches 36; Conservative 4; Mismatches 6; Indels 3; Gaps 2;

QY 28 ICRNRVTNNVNDVKLVANLPKDYMITLKYPGMDVLPSCWISSEMY 76
DB 3 ICRNPVTNDVKITKLVANLPNDYMITLNVVAGMDVLP--WY-DWVIQ 48

Search completed: February 5, 2004, 15:08:21

Job time : 16.4174 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:42:38 ; Search time 8.64876 Seconds
(without alignments)
1484.408 Million cell updates/sec

Title: US-09-224-683-61

Perfect score: 1397

Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISMLQEKEREPOEV 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1397	100.0	273	1 SCF_HUMAN	P21583 homo sapien
2	1219.5	87.3	274	1 SCF_HORSE	Q95md2 equus caball
3	1217.5	87.2	274	1 SCF_FELCA	P79169 felis silve
4	1203.5	86.1	274	1 SCF_PIG	Q29030 sus scrofa
5	1187.5	85.0	274	1 SCF_CARI	Q95m19 capra hircu
6	1184.5	84.8	274	1 SCF_BOVIN	Q28132 bos taurus
7	1180.5	84.5	274	1 SCF_CANFA	Q06220 canis famli
8	1180.5	84.5	274	1 SCF_MUSVI	Q95n18 mustela vis
9	1158	82.9	273	1 SCF_RAT	P21581 rattus norv
10	1157	82.8	273	1 SCF_MOUSE	P20826 mus musculu
11	1156.5	82.8	267	1 SCF_SHEEP	P79368 ovis aries
12	703	50.3	287	1 SCF_CHICK	Q09108 gallus gall
13	702	50.3	287	1 SCF_CONVA	Q90314 coturnix co
14	107.5	7.7	989	1 PTP3_DICDI	P54637 dictyosteli
15	97.5	7.0	983	1 RAGE_MOUSE	Q62151 mus musculu
16	97	6.9	981	1 SCFA_MOUSE	Q94377 rickettsia
17	96.5	6.9	1742	1 MYSC_HUMAN	Q94q44 homo sapien
18	93.5	6.7	1813	1 UN13_CABEL	P27715 caenorhabdi
19	91.5	6.5	496	1 MURE_WIGBR	Q8d21 wiggleswort
20	90.5	6.5	1932	1 FABI_SCHPO	Q59722 schizosacch
21	90	6.4	378	1 FDHA_MERUA	Q60314 methanococc
22	89.5	6.4	384	1 NRPF_HAEIN	P44942 haemophilus
23	89	6.4	282	1 Y218_RICPR	Q05944 rickettsia
24	89	6.4	998	1 SCFA_RICAK	Q94149 rickettsia
25	88.5	6.3	1325	1 YAB6_SCHPO	Q09847 schizosacch
26	88.5	6.3	1875	1 MLPI_YEAST	Q02445 saccharomyc
27	88	6.3	742	1 Y865_MERUA	Q58275 methanococc
28	88	6.3	782	1 YAKH_SCHPO	Q09922 schizosacch
29	87.5	6.3	966	1 CAPF_MERUA	Q02775 schizosacch
30	87	6.2	402	1 RAGE_RAT	Q63455 rattus norv
31	87	6.2	469	1 C39A_HUMAN	Q9ny15 homo sapien
32	87	6.2	664	1 ZAAA_CABEL	Q09543 caenorhabdi
33	87	6.2	844	1 BRO1_YEAST	P48562 saccharomyc

34	87	6.2	1202	1	YE01_SCHPO	O13798 schizosacch
35	86.5	6.2	410	1	ARCA_BORBU	O51781 borrelia bu
36	86.5	6.2	451	1	DNA_PASWU	O9c194 pasteurella
37	86.5	6.2	466	1	DNA_PROMI	P22837 proteus mir
38	86.5	6.2	545	1	VNCS_UCDNV	Q90054 junonia coe
39	86.5	6.2	729	1	CUD6_CABEL	Q21346 caenorhabdi
40	86.5	6.2	1675	1	POL_RTBVP	P27502 rice tungro
41	86.5	6.2	2492	1	TALA_DICDI	P54633 dictyosteli
42	86	6.2	991	1	SCA4_RICAU	Q94j64 rickettsia
43	86	6.2	1146	1	KHMA_DICDI	P42527 dictyosteli
44	86	6.2	2238	1	RRPL_BUNYM	P20470 bunyameira
45	85.5	6.1	344	1	ETPA_YEAST	O12480 saccharomyc

ALIGNMENTS

RESULT 1	ID	SCF_HUMAN	STANDARD:	PRT:	273 AA.
AC	P21583	Q16487; Q9UOK7;			
DT	01-MAY-1991	(Rel. 18, Created)			
DT	01-MAY-1991	(Rel. 18, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).				
GN	KITLG OR MGF OR SCF.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=91004219; PubMed=2208279;				
RA	Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,				
RA	Morris C.F., McNeice I.K., Jacobsen F.W., Mendiaz E.A., Birckett N.C.,				
RA	Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,				
RA	Fisher E.F., Erjavec H.O., Herrera C.J., Wyrzych J., Sachdev R.K.,				
RA	Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zeebo K.M.,				
RT	"Primary structure and functional expression of rat and human stem				
RT	cell factor DNAs."				
RL	Cell 63:203-211(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RX	MEDLINE=99160429; PubMed=10049787;				
RA	Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.,				
RA	"Parathyroid hormone-regulated production of stem cell factor in human				
RT	osteoblasts and osteoblast-like cells."				
RL	Biochem. Biophys. Res. Commun. 255:778-784(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Han C., Peng X., Yuan J., Qiang B.,				
RA	Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.				
RL	[4]				
RP	SEQUENCE OF 167-248 FROM N.A. (ISOFORM 2).				
RX	MEDLINE=92360843; PubMed=1379846;				
RA	Toyota M., Hinoda Y., Itoh F., Tsujisaki M., Inai K., Yachi A.,				
RA	"Expression of two types of kit ligand mRNAs in human tumor cells."				
RL	Int. J. Hematol. 55:301-304(1992).				
CC	-1- FUNCTION: Stimulates the proliferation of mast cells. Able to				
CC	augment the proliferation of both myeloid and lymphoid				
CC	hematopoietic progenitors in bone marrow culture. Mediates also				
CC	cell-cell adhesion. Acts synergistically with other cytokines,				
CC	probably interleukins.				
CC	-1- SUBUNIT: Homodimer, non-covalently linked (Probable).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).				
CC	Also exists as a secreted soluble form (isoform 1 only) (By				
CC	similarity).				
CC	-1- ALTERNATIVE PRODUCTS:				
CC	Event=Alternative splicing; Named isoforms=2;				
CC	Name=1; Synonyms=SCF248;				
CC	Isoid=P21583-1; Sequence=Displayed;				
CC	Name=2; Synonyms=SCF220;				

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CC      IsoId=P21583-2; Sequence=VSP_006022;
CC      -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC      -1- PTM: A soluble form is produced by proteolytic processing of
CC      isoform 1 in the extracellular domain.
CC      -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC      -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC      WWW="http://www.infobiogen.fr/services/chromosome/Genes/MGFD142.html".
CC      -----
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M59964; AAB65450.1; -
DR      EMBL; AF119835; AAD2048.1; -
DR      EMBL; AF400436; AAK92485.1; -
DR      EMBL; AF400437; AAK92486.1; -
DR      EMBL; S42571; AAB22846.2; -
DR      PIR; A35974; A35974.
DR      PIR; B61190; B61190.
DR      Genew; HGNC:6343; KITLG.
DR      NIM; 184745; -
DR      CO; GO:0005173; F:stem cell factor receptor binding activity; TAS.
DR      CO; GO:0008283; P:cell proliferation; TAS.
DR      CO; GO:0007165; P:signal transduction; TAS.
DR      InterPro; IPR003452; SCF.
DR      Pfam; PF02404; SCF; 1.
KW      Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW      Alternative splicing.
FT      SIGNAL 1 25
FT      CHAIN 26 273
FT      DOMAIN 26 214
FT      TRANSMEM 215 237
FT      DISULFID 29 114
FT      CARBOHYD 68 163
FT      CARBOHYD 97 90
FT      CARBOHYD 97 97
FT      CARBOHYD 118 118
FT      CARBOHYD 145 145
FT      CARBOHYD 195 195
FT      VARSPLIC 174 202
FT      FTID=VSP_006022.
FT      CONFLICT 55 55 L -> S (IN REF. 2 AND 3; AAK92486).
FT      CONFLICT 128 128 K -> R (IN REF. 2 AND 3; AAK92486).
FT      CONFLICT 134 134 L -> F (IN REF. 2 AND 3; AAK92486).
SQ      SEQUENCE 273 AA; 30898 MW; 19FD362CB59C6607 CRC64;
Query Match 100.0%; Score 1397; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 3; 7e-100;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      241 QPSLTRAVENTIQTNEEDNEISMLQEKERFQEV 273
|||||
RESULT 2
SCF_HORSE
ID SCF_HORSE STANDARD; PRT; 274 AA.
AC 095MD2; 062765; 095MG8; Q9N1V5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kit ligand precursor (C-Kit ligand) (stem cell factor) (SCF) (mast
DE cell growth factor) (MGF).
GN KITLG OR MGF OR SCF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE OF 4-264 FROM N.A.
RA Terry R.R., Mickelson J.R., Schmutz S., Cottrhan E.G., Bailey E.;
RT "Equus caballus mast cell growth factor (MGF).";
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 12-267 FROM N.A.
RA Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
RT "An Equine sequence homologous to stem cell factor (KIT-ligand).";
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 107-202 AND 227-274 FROM N.A.
RA Terry R.R., Bailey E.F., Cottrhan E.G.;
RT "Evaluation of MGF as the candidate gene for Appaloosa spotting.";
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 147-197 FROM N.A.
RA Caetano A.R., Shue Y.-L., Lyons L.A., Laughlin T.F., O'Brien S.J.,
RA Murray J.D., Bowling A.T.;
RT "A primary human-horse comparative gene map.";
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
CC secreted soluble form (By similarity).
CC -1- PTM: A soluble form is produced by proteolytic processing of
CC the extracellular domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF401625; AAK94474.1; -
DR      EMBL; AF053498; AAC97076.1; -
DR      EMBL; AF637704; AAK63249.1; -
DR      EMBL; AF367706; AAK63250.1; -
DR      EMBL; AF130770; AAK63716.1; -
DR      InterPro; IPR003452; SCF.
DR      Pfam; PF02404; SCF; 1.
KW      Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT      SIGNAL 1 25
FT      CHAIN 26 274
FT      DOMAIN 26 215
FT      TRANSMEM 216 238
FT      DOMAIN 239 274

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FT	DISULFID	29	114	BY SIMILARITY.
FT <th>DISULFID</th> <td>68</td> <td>164</td> <td>BY SIMILARITY.</td>	DISULFID	68	164	BY SIMILARITY.
FT <th>CARBOHYD</th> <td>90</td> <td>90</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	90	90	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <td>97</td> <td>97</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	97	97	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <td>145</td> <td>145</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	145	145	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <td>196</td> <td>196</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	196	196	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <td>207</td> <td>207</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	207	207	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CONFLICT</th> <td>15</td> <td>15</td> <td>Q -> P (IN REF. 2).</td>	CONFLICT	15	15	Q -> P (IN REF. 2).
FT <th>CONFLICT</th> <td>241</td> <td>241</td> <td>MISSING (IN REF. 3).</td>	CONFLICT	241	241	MISSING (IN REF. 3).
SO <th>SEQUENCE</th> <td>274 AA;</td> <td>31217 MM;</td> <td>96C1D4C9059132F2 CRC64;</td>	SEQUENCE	274 AA;	31217 MM;	96C1D4C9059132F2 CRC64;

Query Match	Best Local Similarity	87.3%;	Score 1219.5;	DB 1;	Length 274;
Matches	239;	Conservative	19;	Mismatches	15;
				Indels	1;
				Gaps	1

Qy	1	MKKQTWILTCIYQLLLFNPLVKTGECIRNRVTNNVXDVTGLVANLPEDYMTLTKYVG	60
Db <th>1</th> <th>MKKQTWILTCIYQLLLFNPLVKTGECIRNRVTNDVDVDTGLVANLPEDYMTLTKYVG</th> <th>60</th>	1	MKKQTWILTCIYQLLLFNPLVKTGECIRNRVTNDVDVDTGLVANLPEDYMTLTKYVG	60
Qy <th>61</th> <th>MDVLPSCHWISBMVQVLSDLTDLIDKSNISSEGSNYSIIDKLVNIYDDLVECKENSS</th> <th>120</th>	61	MDVLPSCHWISBMVQVLSDLTDLIDKSNISSEGSNYSIIDKLVNIYDDLVECKENSS	120
Db <th>61</th> <th>MDVLPSCHWISBMVQVLSDLTDLIDKSPNISSEGSNYSIIDKLVNIYDDLVECKEHS</th> <th>120</th>	61	MDVLPSCHWISBMVQVLSDLTDLIDKSPNISSEGSNYSIIDKLVNIYDDLVECKEHS	120
Qy <th>121</th> <th>KDLKSPSPPEPLTPEPEPFIRNRSIDAFKDF-VVASSETSDCVVSTLSEPKDSRVSV</th> <th>179</th>	121	KDLKSPSPPEPLTPEPEPFIRNRSIDAFKDF-VVASSETSDCVVSTLSEPKDSRVSV	179
Db <th>121</th> <th>ENVKSYSSQESRLTPEPEPFIRNRSIDAFKDLNVVSKSECVVSTLSEPKDSRVSV</th> <th>180</th>	121	ENVKSYSSQESRLTPEPEPFIRNRSIDAFKDLNVVSKSECVVSTLSEPKDSRVSV	180
Qy <th>180</th> <th>TKPEMLPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALPSLIIIGFAGALYMKK</th> <th>239</th>	180	TKPEMLPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALPSLIIIGFAGALYMKK	239
Db <th>181</th> <th>TKPEMLPVAASSLRNDSSSNRKAKNSNTGDSNLQMAAMALPALPSLIVIGFAGALYMKK</th> <th>240</th>	181	TKPEMLPVAASSLRNDSSSNRKAKNSNTGDSNLQMAAMALPALPSLIVIGFAGALYMKK	240
Qy <th>240</th> <th>ROPSLTRAVENIQINEEDNEISMLOEKEREFOEV</th> <th>273</th>	240	ROPSLTRAVENIQINEEDNEISMLOEKEREFOEV	273
Db <th>241</th> <th>KOPNLTRAVENIQINEEDNEISMLOEKEREFOEV</th> <th>274</th>	241	KOPNLTRAVENIQINEEDNEISMLOEKEREFOEV	274

RESULT 3	SCF_FELICA	STANDARD;	PRT;	274 AA.
AC	P79169;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).			
GN	KITLG OR SCF.			
OS	Felis silvestris catus (Cat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.			
OX	NCHI_TaxID=9685;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RX	MEDLINE=97069946; PubMed=8912926;			
RA	Dunham S.P., Onions D.E.;			
RT	"The cloning and sequencing of cDNAs encoding two isoforms of feline stem cell factor."			
RL	DNA Seq. 6:233-237(1996).			
CC	-1- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).			
CC	-1- SUBUNIT: Homodimer, non-covalently linked (Probable).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2). Also exists as a secreted soluble form (isoform 1 only) (By similarity).			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	Isoid=P79169-1; Sequence=Displayed;			
CC	Name=2;			
CC	Isoid=P79169-2; Sequence=VSP_006021;			
CC	-1- PTM: A soluble form is produced by proteolytic processing of			

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CC isoform 1 in the extracellular domain (By similarity).
CC - - - SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
DR EMBL; D50833; BAA09445.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; signal; Cell adhesion;
KW Alternative splicing.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 274 KIT LIGAND.
FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 216 238 POTENTIAL.
FT DOMAIN 239 274 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 114 BY SIMILARITY.
FT DISULFID 68 164 BY SIMILARITY.
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 175 203 DSRVSVKPPMLPPVAASSLRNDSSSNR -> G (1n
isoform 2).
FT FT /FTId:VSP_006021.
SQ SEQUENCE 274 AA; 30987 MW; C5B78DB4791237BE CRC64;
Query Match 87.2%; Score 1217.5; DB 1; Length 274;
Best Local Similarity 87.2%; Pred. No. 2.1e-86;
Matches 239; Conservative 17; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKKTQWTLTCIYQLLFFNPVLTSGICNNRRVTNNVQDYTKLVANPKQYMTLTQYVP 60
DB 1 MKKTQWTLTCIYQLLFFNPVLTSGICNNRRVTNNVQDYTKLVANPKQYMTLTQYVP 60
QY 61 MDVLPSSHCHTSEMWVOLSDSLTDLDFKSNISSEGLSNYSYIIDKLVNIVDDLVEGVKSNSS 120
DB 61 MDVLPSSHCHTSEMWVOLSDSLTDLDFKSNISSEGLSNYSYIIDKLVNIVDDLVEGVKSNSS 120
QY 121 KDLKKFSKSEPEPLFTPEEFPRIFNRSIDAFKDF-VVASETSDCVSVSTLSPKDSRVSV 179
DB 121 ENYKSSKSEPEPLFTPEEFPRIFNRSIDAFKDLQEMVASTSECVSVSTLSPKDSRVSV 180
QY 180 TKCPMLPPVAASSLRNDSSSNRKAQNPQDSSLIHMAAMLPALFSIIIGFAGALYWK 239
DB 181 TKCPMLPPVAASSLRNDSSSNRKAQNPIDSSIGMAVMALPACFSIVIGAFGAFYWK 240
QY 240 RQPSLTVAENIQINEEDNISMLOEKERKFOEV 273
DB 241 RQPSLTVAENIQINEEDNISMLOEKERKFOEV 274
RESULT 4
SCF_PIG STANDARD; PRT; 274 AA.
AC Q29030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
cell growth factor) (MGF).
GN KITLG OR MGF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9623;
NN [1]
SEQUENCE FROM N.A.

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RC	TX	TISSUE=uterus;	PUBMED=94146218; PubMed=7508758;
RA	Zhang Z., Anthony R.V.;	"Porcine stem cell factor/c-kit ligand: its molecular cloning and localization within the uterus.";	
RT	Biol. Reprod. 50:95-102(1994).		
RL			
CC	- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).		
CC	- SUBUNIT: Homodimer, non-covalently linked (Probable).		
CC	- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).		
CC	- Ptm: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).		
CC	- SIMILARITY: BELONGS TO THE SCF FAMILY.		
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC			
DR	EMBL; L07786; AAA53670.1; -.		
DR	PIR; I46575; I46575.		
DR	InterPro; IPR003452; SCF.		
DR	Pfam; PF02404; SCF; 1.		
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.		
FT	SIGNAL	1 25	BY SIMILARITY.
FT	CHAIN	26 274	KIT LIGAND.
FT	DOMAIN	26 215	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	216 238	POTENTIAL.
FT	DOMAIN	239 274	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	29 114	BY SIMILARITY.
FT	DISULFID	68 164	BY SIMILARITY.
FT	CARBOHYD	90 90	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	97 97	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	145 145	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	196 196	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	274 AA; 3118 MW; FP3C87114D7BA6A6 CRC64;	
Query Match	Best Local Similarity	86.1%; Score 1203.5; DB 1; Length 274;	
Matches 235; Conservative	22; Mismatches 16; Indels 1; Gaps 1;		
QY	1 MKKTQWTWLTCTIYQQLFNPFLVYKTEGICRRNRVYNNVQDVKLVANLPKDYMITLKYPG	60	
DB	1 MKKTQWTWLTCTIYQQLFNPFLVYKTEGICRRNRVYNNVQDVKLVANLPKDYMITLKYPG	60	
QY	61 MDVLPSSHCHWISSEMYVQVSDSLTDLDDKRSNISEGLSNYSIIDKLVNIYDDIVEGCKENSS	120	
DB	61 MDVLPSSHCHWISSEMYVQVSDSLTDLDDKRSNISEGLSNYSIIDKLVNIYDDIVEGCKENSS	120	
QY	121 KDLKKSFKSPPEPLRFTPEEPRFIRFNRSIDAEKDFVVASSETSDCVSSSTLSPKDSRVS	179	
DB	121 ENVKSSKSPPEPLRFTPEEPRFIRFNRSIDAEKDFVVASSETSDCVSSSTLSPKDSRVS	180	
QY	180 TKPFLMLPVVAASSLRNDSSSSNRKAKNDPGGSSLHMAAMALPALFSLTIGAFGALYWK	239	
DB	181 TKPFLMLPVVAASSLRNDSSSSNRKAKNDPGGSSLHMAAMALPALFSLTIGAFGALYWK	240	
QY	240 RQPSLTRAVENTIQTNEEDNEISMLQEKREPOEV	273	
DB	241 KQPSLTRAVENTIQTNEEDNEISMLQEKREPOEV	274	
RESULT 5	ID SCF_CAPH1	STANDARD; PRT; 274 AA.	
NC	Q95MI19;		

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
DE Cell ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
DE KITLG OR SCF.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Shiba; TISSUE=Brain;
RA Yamagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;
RT "Identification of splicing isoforms of caprine stem cell factor
RT (gSCF) transcripts and expression patterns of the two major isoforms,
RT gSCF825 and gSCF741, in the brain and the skin of adult and fetal
RT Shiba goats. Capra hircus.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -I- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
CC secreted soluble form (By similarity).
CC -I- PTM: A soluble form is produced by proteolytic processing of
CC the extracellular domain (By similarity).
CC -I- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
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CC -----
DR EMBL; AB002152; BAB71753.1; -.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25
FT CHAIN 26 274
FT DOMAIN 26 215
FT TRANSMEM 216 238
FT DOMAIN 239 274
FT DISULFID 29 114
FT DISULFID 68 164
FT CARBOHYD 90 90
FT CARBOHYD 97 97
FT CARBOHYD 145 145
FT CARBOHYD 196 196
SQ SEQUENCE 274 AA; 31052 MW; BBE669A09EF65D CRC64;
Query Match 85.0%; Score 1187.5; DB 1; Length 274;
Best Local Similarity 85.0%; Pred. No. 4.3e-84;
Matches 233; Conservative 20; Mismatches 20; Indels 1; Gaps 1
QY 1 MKKTQTMILTCIYQLLLFNPLVTEGICRNRVTNNVADVTKLVANLPKQYMITLKYPG 60
DB 1 MKKTQTMILTCIYQLLLFNPLVHSGICRNRVTVDVADVTKLVANLPKQYMITLKYPG 60
QY 61 MDVLPSCWISSENVVQVSDSLTDLIDKFRSNISEGLSNYSIIDKLVNYVDLVECYKENSS 120
DB 61 MDVLPSCWISSENVQVSLTDLIDKFRSNISEGLSNYSIIDKLVKYVDLVECYKEHSF 120
QY 121 KDLKKSFSPEPLRFTPEEPRIFNRSIDAFKDF-VVASETSPDCVASTLSPEKDSRVSY 179
DB 121 ENVAKSKSPPEPRTPEKFFGILNKSIDAFKDLFIYASTMSSECVISTSSPEKDSRVSY 180

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Oy	180	TKPMLPVPVAAASSLRNDSSSSNRKAKNPPGSSSLHMAAMALPALFSLIIGAPALWYKK	233
Db	181	TKPMLPVPVAAASSLRNDSSSSNRKAKNPPGSSSLHMAAMALPALFSLIIGAPALWYKK	240
Oy	240	RQPSLTRAVENTIQINEEDNEISMLQEKERPEQEV	273
Db	241	KQPLULTRVENVQINEEDNEISMLQEKERPEQEV	274
RESULT 6			
ID	SCF_BOVIN	STANDARD;	PRT; 274 AA.
AC	Q28132;	Q9TU74;	
DT	28-FEB-2003	(Rel. 41, Created)	
DT	28-FEB-2003	(Rel. 41, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	Kit 1lgand precursor (C-kit 1lgand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).		
GN	KITLG OR SCF.		
OS	Bos taurus (bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RC	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
RC	TISSUE=Spleen;		
RX	MEDLINE=94339176; PubMed=7520283;		
RA	Zhou J., Hikono H., Ohtaki M., Kubota T., Sakurai M.;		
RT	"Cloning and characterization of cDNAs encoding two normal isoforms of bovine stem cell factor.";		
RL	Biochim. Biophys. Acta 1223:148-150(1994).		
RN	[2]		
RC	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE=Fetal brain;		
RA	Kudo T.;		
RT	"Bovine counterpart of stem cell factor.";		
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RC	SEQUENCE OF 204-239 FROM N.A., AND VARIANT ASP-218.		
RC	STRAIN=Belgian Blue;		
RX	MEDLINE=99315331; PubMed=10384045;		
RA	Seitz J.U., Schmutz S.M., Thue T.D., Buchanan F.C.;		
RT	"A missense mutation in the bovine MGF gene is associated with the roan phenotype in Belgian Blue and Shorthorn cattle.";		
RL	Mamm. Genome 10:710-712(1999).		
CC	-1- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).		
CC	-1- SUBUNIT: Homodimer, non-covalently linked (Probable).		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2). Also exists as a secreted soluble form (isoform 1 only) (By similarity).		
CC	-1- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=2;		
CC	Name=1;		
CC	IsoId=Q28132-1; Sequence=Displayed;		
CC	Name=2;		
CC	IsoId=Q28132-2; Sequence=VSP_006020;		
CC	-1- PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain (By similarity).		
CC	-1- POLYMORPHISM: The Roan locus is responsible for the coat coloration of Belgian Blue and Shorthorn cattle. The solid-colored and white animals are homozygotes, and the roan animals, with intermingled colored and white hairs, are heterozygous. The roan phenotype is due to the Asp-218 mutation.		
CC	-1- SIMILARITY: BELONGS TO THE SCF FAMILY.		
CC	-----		
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-----  
DR EMBL; D8934; BAA06061.1; -.  
DR DR EMBL; AB033716; BAAG94808.1; -.  
DR EMBL; AF120154; AAD55355.1; -.  
DR PIR; S47571; S47571.  
DR InterPro; IPR003452; SCF.  
KM Pfam; PF02404; SCF. 1.  
DR Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;  
KW Alternative splicing; Polymorphism.  
FT SIGNAL  
   1              25  
FT CHAIN  
   26    274  
FT DOMAIN  
   26        215  
FT TRANSMEM  
   216        238  
FT DOMAIN  
   239        274  
FT DISULFD  
   29        114  
FT DISULFD  
   68        164  
FT CARBOHYD  
   90        90  
FT CARBOHYD  
   145        145  
FT CARBOHYD  
   196        196  
FT VASPLIC  
   175        203  
  
isoform 2).  
/ftid=VSP_006020.  
A -> D (IN ROAN).  
SQ SEQUENCE   218 AA;   218 MM;   DECIDDB7B0CB12B CRC64;  
  
Query Match                   84.8%; Score 1184.5; DB 1; Length 274;  
Best Local Similarity       84.7%; Pred. No. 7,3e-84;  
Matches 232; Conservative 20; Mismatches 21; Indels 1; Gaps 1;  
  
QY    1 MKKTQTWILTCIYLQLLFNPLVTESICGNRVTVNNKDVTKLVANTPKDYMITLKATYPG 60  
Db    1 MKKTQTWITLCIYLQLLFNPLVHTSGICSNRTVDVKDTKLVAALPKDYMITLKATYPG 60  
  
QY    61 MDVLPSHCWISEMVVVSDSLTDLDFNSISEGLSNYSIIIDKLVIIVDDLVECVKENSS 120  
Db    61 MDVLPSHCWISIEWEQSVSUTLDLDFSNSISEGLSNVCIIIDKLKIIVDDIVECMEBSHS 120  
  
QY    121 KDLKKSKRSSTPRLPTTEEPFRPIFNKSIDAFAKP-VVASETSDCVASTLSPEKDTSVS 179  
   :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db    121 ENYYKSSSKSPBPQTFEKEFFGFNFKSIDAFKDEIVAASKSECVISTSPEDSRVS 180  
  
QY    180 TKRPMLPPVAASSLRNDSSSNRKAQPGGSLLHMAAMLPALFSLTIGAPGALTWK 239  
Db    181 TKRPMLPPVAASSLRNDSSSNRKASIEDSSIOMAVALLPAFLSYLGAFGAFYMK 240  
  
QY    240 RQPSSLRAVENIQINEEDNEISMLOEKEREFOEV 273  
   ||:||:|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db    241 KPPLYTRTYENROINEDNEISMLOEKEREFQEV 274  
  
RESULT 7  
SCF CANFA STANDARD; PRt; 274 AA.  
AC O06220; OSBPM6;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast  
cell growth factor) (MGF).  
NCBI_King OR MGf.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI_TaxId=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=T-cell;  
EA MEDLINE=93106145; PubMed=1281786;  
RA Shull R.M., Sugus S.V., Langley K.E., Okino K.H., Jacobsen F.W.
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Query Match	84.5%	Score 1180.5	DB 1	Length 274
Best Local Similarity	85.4%	Pred. No. 1.5e-83		
Matches 234	Conservative 17	Mismatches 22	Indels 1	Gaps 1
RA	Marlin F.H.:			
RT	"Canine stem cell factor (c-kit ligand) supports the survival of			
RT	hematopoietic progenitors in long-term canine marrow culture."			
RL	Exp. Hematol. 20:1118-1124(1992).			
RN	[12]			
RP	SEQUENCE OF 17-274 FROM N.A.			
RA	TISSUE=Tail;			
RC	Schmutz S.M., Berryere T.G.:			
RT	"MCG sequencing in the dog aids in mapping to CPAL5."			
RL	Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.			
CC	- FUNCTION: Stimulates the proliferation of mast cells. Able to			
CC	augment the proliferation of both myeloid and lymphoid			
CC	hematopoietic progenitors in bone marrow culture. Mediates also			
CC	cell-cell adhesion. Acts synergistically with other cytokines,			
CC	probably interleukins.			
CC	- SUBUNIT: Homodimer, non-covalently linked (Probable).			
CC	- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a			
CC	secreted soluble form.			
CC	- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.			
CC	- PFM: A soluble form is produced by proteolytic processing of			
CC	the extracellular domain (by similarity).			
CC	- SIMILARITY: BELONGS TO THE SCF FAMILY.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; S53329; AAB24619.1; -			
DR	EMBL; AY094361; AAM16280.1; -			
DR	PIR; I46929; I46929.			
DR	InterPro; IPR003452; SCF.			
DR	Pfam; PF02404; SCF; 1.			
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.			
FT	SIGNAL	1	25	BY SIMILARITY.
FT	CHAIN	26	274	KIT LIGAND.
FT	DOMAIN	26	215	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	216	238	POTENTIAL.
FT	DOMAIN	239	274	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	29	114	BY SIMILARITY.
FT	DISULFID	68	164	BY SIMILARITY.
FT	CARBOHYD	90	90	N-LINKED (GLYCANC. . .) (POTENTIAL).
FT	CARBOHYD	97	97	N-LINKED (GLYCANC. . .) (POTENTIAL).
FT	CARBOHYD	145	145	N-LINKED (GLYCANC. . .) (POTENTIAL).
FT	CARBOHYD	196	196	N-LINKED (GLYCANC. . .) (POTENTIAL).
SQ	SEQUENCE	274 AA;	30869 MW;	4182B9AED00793B CRC64;

RESULT 8	ID	SCF MUSVI	STANDARD;	PRT;	274 AA.
AC	Q95N18; Q95NM5;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Kit ligand precursor, (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).				
DE	cell growth factor) (MGF).				
GN	KITLG OR SCF.				
OS	Mustela vison (American mink).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;				
OC	Mustela.				
OX	NCBI_TaxID=9667;				
RA	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RL	Bennett R.D., Murphy B.D.;				
CC	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.				
CC	- FUNCTION: Stimulates the proliferation of mast cells. Able to				
CC	augment the proliferation of both myeloid and lymphoid				
CC	hematopoietic progenitors in bone marrow culture. Mediates also				
CC	cell-cell adhesion. Acts synergistically with other cytokines,				
CC	probably interleukins (By similarity).				
CC	- SUBUNIT: Homodimer, non-covalently linked (Probable).				
CC	- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a				
CC	secreted soluble form (By similarity).				
CC	- ALTERNATIVE PRODUCTS:				
CC	Event=Alternative splicing; Named isoforms=2;				
CC	Name=1;				
CC	Isoid=Q95N18-1; Sequence=Displayed;				
CC	Name=2;				
CC	Isoid=Q95N18-2; Sequence=VSP_006024;				
CC	- PTM: A soluble form is produced by proteolytic processing of				
CC	isoform 1 in the extracellular domain (By similarity).				
CC	- SIMILARITY: BELONGS TO THE SCF FAMILY.				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AY013712; AACG7434.1; -				
DR	EMBL; AF333757; AAK73366.1; -				
DR	InterPro; IPR003452; SCF.				
DR	Pfam; PF02404; SCF; 1.				
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;				
KW	Alternative splicing.				
KW	SIGNAL	1	25		
FT	CHAIN	26	274		
FT	DOMAIN	26	215		
FT	TRANSMEM	216	238		
FT	DOMAIN	239	274		
FT	DISULFID	29	114		
FT	DISULFID	68	164		
FT	CARBOHYD	90	90		
FT	CARBOHYD	97	97		
FT	CARBOHYD	145	145		
FT	CARBOHYD	196	196		
FT	VASAPLIC	175	203		
FT					
FT					
FT					
FT	CONFLICT	65	65		
FT	CONFLICT	171	171		
FT	CONFLICT	268	274		
FT					
FT	SEQUENCE	274 AA;	31034 MW;	SAC1619014A5E72 CRC64;	

QY 181 KPFLPVPVAASSLRNDSSSNRKAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 240
 DB 181 KPFLPVPVAASSLRNDSSSNRKAAXSPEDPGLQWTAMLPALISLIVIGFAGALYMKK 240
 QY 241 QPSLTRAVENTIQNEEDNEISMLQEKEREFQEV 273
 DB 241 QSSLTRAVENIQNEEDNEISMLQOKEREFQEV 273
 RESULT 10
 SCF_MOUSE STANDARD; PRT; 273 AA.
 ID SCF_MOUSE
 AC F20826; P97332; Q62524; Q64222; Q921N5;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast cell growth factor) (MGF) (hematopoietic growth factor KL) (Steel factor).
 GN KITLG OR KITL OR MGF OR SL OR SLF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=MCB6F1;
 RX MEDLINE=91004223; PubMed=1698558;
 RA Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Bisenman J., Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D., Williams D.E.;
 RA "Molecular cloning of mast cell growth factor, a hematopoietin that is active in both membrane bound and soluble forms.";
 RL Cell 63:1235-243 (1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=92330001; PubMed=1378327;
 RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
 RA "Differential expression and processing of two cell associated forms of the kit-ligand: KL-1 and KL-2";
 RL Mol. Biol. Cell 3:349-362 (1992).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=MCB6F1;
 RX MEDLINE=91160046; PubMed=1705866;
 RA Flanagan J.G., Chan D.C., Leder P.;
 RA "Transmembrane form of the kit ligand growth factor is determined by alternative splicing and is missing in the Slid mutant.";
 RL Cell 64:1025-1035 (1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=93012940; PubMed=1383087;
 RA Branman C.T., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A., Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A., Copeland N.G.;
 RA "Developmental abnormalities in Steel^{17H} mice result from a splicing defect in the steel factor cytoplasmic tail.";
 RL Genes Dev. 6:1832-1842 (1992).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J;
 RX MEDLINE=97002551; PubMed=8849898;
 RA Bedell M.A., Copeland N.G., Jenkins N.A.;
 RA "Multiple pathways for Steel regulation suggested by genomic and sequence analysis of the murine Steel gene.";
 RL Genetics 142:927-934 (1996).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS PRO-193 AND SER-207.
 RC STRAIN=C3H/EL; TISSUE=Brain;
 RX MEDLINE=97032534; PubMed=8875893;
 RA Graw J., Loester J., Neuhäuser-Klaus A., Pretsch W., Schmitt-John T.;
 RA "Molecular analysis of two new Steel mutations in mice shows a

RT transversion or an insertion.";
 RL Mamm. Genome 7:843-846 (1996).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS SER-122; PRO-193 AND SER-207.
 RC STRAIN=102/El x C3H/El;
 RX MEDLINE=98025115; PubMed=9360640;
 RA Graw J., Neuhäuser-Klaus A., Pretsch W.;
 RA "Detection of a point mutation (A to G) in exon 5 of the murine Mgf gene defines a novel allele at the Steel locus with a weak phenotype.";
 RL Mutat. Res. 382:75-78 (1997).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Toh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuwaji P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombereis P., Noriote P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmig L., Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S., Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SER-207.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Bladesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [10]
 RP SEQUENCE OF 1-270 FROM N.A. (ISOFORM 1), AND SEQUENCE OF 26-65.
 RX MEDLINE=91004221; PubMed=1698557;
 RA Hung E., Nocka K., Beier D.R., Chu T.Y., Buck J., Lahm H.W., Wellner D., Leder P., Besmer P.;
 RA "The hematopoietic growth factor KL is encoded by the Sl locus and is the ligand of the c-kit receptor, the gene product of the W locus.";
 RL Cell 63:225-233 (1990).
 RN [11]
 RP SEQUENCE OF 1-201 FROM N.A.
 RX MEDLINE=91004220; PubMed=1698556;
 RA Zsebo K.M., Williams D.A., Geissler E.N., Broudy V.C., Martin F.H., Atkins H.L., Hsu R.-Y., Birkett N.C., Okino K.H., Mudrock D.C., Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattaneach B.M.,

RA Galli S.J., Suggs S.V.;
 RT "stem cell factor is encoded at the Sl locus of the mouse and is the
 RT ligand for the c-kit tyrosine kinase receptor."
 RL Cell 63:213-224(1990).
 RN [12]
 RP SEQUENCE OF 26-53.
 RX MEDLINE=91004216; Pubmed=1698554;
 RA Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A.,
 RA Cosman D., Anderson D., Lyman S.D., Williams D.E.;
 RT "Mast cell growth factor maps near the steel locus on mouse
 RT chromosome 10 and is deleted in a number of steel alleles."
 RL Cell 63:175-183(1990).
 RN [13]
 RP PARTIAL SEQUENCE OF 26-78.
 RX MEDLINE=91004215; Pubmed=1698553;
 RA Williams D.E., Eisenman J., Baird A., Rauch C., van Ness K.,
 RA March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S.,
 RA Burgess G.S., Cosman D., Lyman S.D.;
 RT "Identification of a ligand for the c-kit proto-oncogene."
 RL Cell 63:167-174(1990).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins.
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
 CC Also exists as a secreted soluble form (isoform 1 only) (by
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=KL-1;
 CC IsoId=P20826-1; Sequence=displayed;
 CC Name=2; Synonyms=KL-2;
 CC IsoId=P20826-2; Sequence=VSP_006023;
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC isoform 1 in the extracellular domain.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 DR EMBL; M59915; AAA40095.1; -
 DR EMBL; M57647; AAA39538.1; -
 DR EMBL; S40534; AAB22555.2; -
 DR EMBL; X69989; CAA48778.1; -
 DR EMBL; U44724; -; NOT ANNOTATED_CDS.
 DR EMBL; U44725; AAC52447.1; -
 DR EMBL; X95381; CAA64667.1; -
 DR EMBL; X99322; CAA67698.1; -
 DR EMBL; Y10287; CAA71329.1; -
 DR EMBL; AK018777; BAB31402.1; -
 DR EMBL; BC011322; AAB11322.1; -
 DR EMBL; S40364; AAB22554.2; -
 DR EMBL; M59912; AAA39539.1; -
 DR PIR; A37934; A37934.
 DR PIR; S65801; S65801.
 DR MGD; MGI:96974; Kiti1.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 Query March 82.8%; Score 1157; DB 1; Length 273;
 Best Local Similarity 82.8%; Pred. No. 9.3e-82;
 Matches 226; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 1 MKKTQWITLCITVQLLEPNLVKTEGICRNRVNNVADVTKLVANLPKDMITLTKVPV 60
 DB 1 MKKTQWITLCITVQLLEPNLVKTEGICRNRVNNVADVTKLVANLPKDMITLTKVPV 60

QY 61 MDVPSHCWISBMMVYQLSDSLTDLDFKSNISEGLSNYSIIDKLVNIYDDLVECVKENS 120
 DB 61 MDVPSHCWISBMMVYQLSDSLTDLDFKSNISEGLSNYSIIDKLVNIYDDLVECVKENS 120

QY 121 KDLKSPKSPBEPRLFTPEEFRIENRSIDAFKDPVVASETDVCVSTLSPKDSRVST 180
 DB 121 KDLKSPKSPBEPRLFTPEEFRIENRSIDAFKDPVVASETDVCVSTLSPKDSRVST 180

QY 121 KNIKSPKRPETRSPTPEEFISIFNRSIDAFKDPVVASETDVCVSTLSPKDSRVST 180
 DB 121 KNIKSPKRPETRSPTPEEFISIFNRSIDAFKDPVVASETDVCVSTLSPKDSRVST 180

QY 181 KPFMLPVAASSLRNDSSSNKAKNPEDSSSLHMAANLPLFLLIGFAGALYMKR 240
 DB 181 KPFMLPVAASSLRNDSSSNKAKNPEDSSSLHMAANLPLFLLIGFAGALYMKR 240

QY 241 OPSLRAVENIQINEDNISMWLOEKERFOEV 273
 DB 241 OPSLRAVENIQINEDNISMWLOEKERFOEV 273

RESULT 11
 SCF SHEEP
 ID - SCF SHEEP STANDARD; PRT; 267 AA.
 AC P79368; Q28591;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
 DE cell growth factor) (MGP) (fragment).
 GN KITLG OR SCF.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxId=9940;
 RN [1]
 RP SEQUENCE OF 8-267 FROM N.A.
 RC TISSUE=ovarian follicle;
 RX MEDLINE=96413880; Pubmed=8662240;
 RA Tisdall D.J., Quirke L.D., Galloway S.M.;
 RT "Ovine stem cell factor gene is located within a syntenic group on
 RT chromosome 3 conserved across mammalian species."
 RL Mamm. Genome 7:472-473(1996).
 RN [2]
 RP SEQUENCE OF 1-202 FROM N.A.
 RA McInnes C.J., Logan M., Falconer V.M., Rawlins P., Huntly J., Haig D.;
 RT "Molecular cloning and biological activity of ovine stem cell
 RT factor."
 RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins (by similarity).
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
 CC secreted soluble form (by similarity).
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC the extracellular domain (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 DR EMBL; U89874; AAB69491.1; -
 DR EMBL; Z50743; CAA90620.1; -
 DR PIR; S58313; S58313.
 DR InterPro; IPR003452; SCF.
 DR Pfam; PF02404; SCF_1.
 KM Growth factor; Glycoprotein; Transmembrane; signal; Cell adhesion.


```
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 >267 KIT LIGAND.
FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 POTENTIAL.
FT DOMAIN 239 >267 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 114 BY SIMILARITY.
FT DISULFID 68 164 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 267 267
SQ SEQUENCE 267 AA; 30148 MW; 9090959549BEC841 CRC64;

Query Match 82.8%; Score 1156.5; DB 1; Length 267;
Best Local Similarity 85.0%; Pred. No. 9,9e-82;
Matches 227; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVTEGICNRRVNNVKDVKLVANLPKDYMTTLKYVPG 60
1 MKKTQWILTCIYLQLLFNPLVTEGICNRRVNNVKDVKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWILTCIYLQLLFNPLVTEGICNRRVNNVKDVKLVANLPKDYMTTLKYVPG 60
QY 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISEGLSNYSIIDKLVINIYDDLYECVKEKNS 120
61 MDVLPSCWISSEWVQSLDLDLDFKFSNISEGLSNYSIIDKLVINIYDDLYECVKEKNS 120
DB 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISEGLSNYSIIDKLVINIYDDLYECVKEKNS 120
QY 121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDF-VVASETDCVVSSTLSPEKDSRVAV 179
121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDF-VVASETDCVVSSTLSPEKDSRVAV 179
DB 121 ENVKSKSKSEPEQPFPEKFEFGIFNKSIDAFKDLLEIVASMSVCVSISSSPKDSRVAV 180
QY 180 TKRFPMLPVAASSLRNDSSSNRKANPPGSSLSHMAAMALPALFSLIIGFAFGALYMK 239
180 TKRFPMLPVAASSLRNDSSSNRKANPPGSSLSHMAAMALPALFSLIIGFAFGALYMK 239
DB 181 TKRFPMLPVAASSLRNDSSSNRKANSIEDSSLSQAAVALPAFFSLVIGFAFGALYMK 240
QY 240 RQPSLTRAVENTIOINEEDNEISMLOEK 266
240 RQPSLTRAVENTIOINEEDNEISMLOEK 266
DB 241 KQPLTRTVENRQINEEDNEISMLOEK 267

RESULT 12
SCF_CHICK STANDARD; PRT; 287 AA.
ID SCF_CHICK
AC Q09108;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGP).
GN KITLG OR SCF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OC NCBI_TaxID=9031;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=93273244; PubMed=7684722;
RA Zhou J., Ohtaki M., Sakurai M.;
RT "Sequence of a cDNA encoding chicken stem cell factor.";
RL Gene 127:269-270(1993).
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hemopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).
CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -1- PTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC -----
DR EMBL, D13516; BAA02733.1; -.
DR PIR, J06037; J06037.1; -.
DR InterPro, IPR003452; SCF.
DR Pfam, PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 287 KIT LIGAND.
FT DOMAIN 26 225 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 226 246 POTENTIAL.
FT DOMAIN 247 287 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 117 BY SIMILARITY.
FT DISULFID 68 167 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 287 AA; 32328 MW; 6AE8556ADC152578 CRC64;

Query Match 50.3%; Score 703; DB 1; Length 287;
Best Local Similarity 51.9%; Pred. No. 6,4e-47;
Matches 149; Conservative 50; Mismatches 74; Indels 14; Gaps 6;

QY 1 MKKTQWILTCIYLQLLFNPLVTEGICNRRVNNVKDVKLVANLPKDYMTTLKYVPG 60
1 MKKTQWILTCIYLQLLFNPLVTEGICNRRVNNVKDVKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWILTCIYLQLLFNPLVTEGICNRRVNNVKDVKLVANLPKDYMTTLKYVPG 60
QY 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISEGLSNYSIIDKLVINIYDDLYECVKE 117
61 MDVLPSCWISSEWVQSLDLDLDFKFSNISEGLSNYSIIDKLVINIYDDLYECVKE 117
DB 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISEGLSNYSIIDKLVINIYDDLYECVKE 117
QY 118 NSSKD-LKSKFSPEPRLFTPEEFRIENRSIDAFKDFVVASETDCVVSSTLSPEKDS 175
118 NSSKD-LKSKFSPEPRLFTPEEFRIENRSIDAFKDFVVASETDCVVSSTLSPEKDS 175
DB 121 DKNDQFENKGNHLYEEDFIPENFRLFNSTIEYKKEADLDNDCTMPETVEPENS 180
QY 176 RVSVTKRPPMLPVAASSLRNDSSSNRKANPPGSSLSHMAAMALPALFSLIIG 229
176 RVSVTKRPPMLPVAASSLRNDSSSNRKANPPGSSLSHMAAMALPALFSLIIG 229
DB 181 RVALTKTISFPVAASSLRNDSSSNRKANPPGSSLSHMAAMALPALFSLIIG 240
QY 220 FAFGLYMKRQRP-SLTRAVENTIOIN--EENNEISMLOEKREPOEV 273
220 FAFGLYMKRQRP-SLTRAVENTIOIN--EENNEISMLOEKREPOEV 273
DB 241 FILGATYMKKTHPKSRPESNETIOCHGQEESEISMLOEKKEHLYQV 287

RESULT 13
SCF_COTUA STANDARD; PRT; 287 AA.
ID SCF_COTUA
AC Q90314; Q90315;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGP).
GN KITLG OR SCF.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
OC NCBI_TaxID=93934;
RN [1]
RX SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=96283808; PubMed=8679698;
RA Petite J.N., Kulik M.J.;
RT "Cloning and characterization of cDNAs encoding two forms of avian stem cell factor.";
RL Biochim. Biophys. Acta 1307:149-151(1996).
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
```



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CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (by similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
CC Also exists as a secreted soluble form (isoform 1 only) (By
CC similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=2:
CC     Name=1;
CC     IsoId=Q90314-1; Sequence=Displayed;
CC     Name=2;
CC     IsoId=Q90314-2; Sequence=VSP_006026;
CC -1- PTM: A soluble form is produced by proteolytic processing of
CC isoform 1 in the extracellular domain.
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC -----
DR EMBL; UA3078; AAC59933.1; -
DR EMBL; UA3079; AAC59934.1; -
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 287
FT DOMAIN 26 225
FT TRANSMEM 226 246
FT DOMAIN 247 287
FT DISULFID 29 117
FT DISULFID 68 167
FT CARBOHYD 100 100
FT CARBOHYD 106 106
FT CARBOHYD 149 149
FT CARBOHYD 178 178
FT CARBOHYD 200 200
FT CARBOHYD 206 206
FT VARSELIC 179 213
FT FT
FT FT
SQ SEQUENCE 287 AA; 32455 MW; ABA81AER422A702E CRC64;

Query Match 50.3%; Score 702; DB 1; Length 287;
Best Local Similarity 51.6%; Pred. No. 7,7e-47;
Matches 148; Conservative 51; Mismatches 74; Indels 14; Gaps 6;

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RESULT 14
PTP3_DICD1
ID PTP3_DICD1 STANDARD; PRT; 989 AA.
AC P54637;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (Protein-tyrosine-
DE phosphate phosphatase 3).
GN (PTPCL OR PTP3) AND (PTPCL OR PTP3).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxId=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RX MEDLINE=96189126; PubMed=8628311;
RA Gampert M., Howard P.K., Hunter T., Firtel R.A.;
RT "Multiple roles of the novel protein tyrosine phosphatase PTP3 during
RT Dictyostelium growth and development.";
RL Mol. Cell. Biol. 16:2431-2444 (1996).
CC -1- FUNCTION: SEEMS TO DEPHOSPHORYLATE A PROTEIN OF 130 kDa (P130).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: IN THE ANTERIOR-LIKE AND PRESTALK CELL TYPES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT MODERATE LEVELS DURING GROWTH
CC AND DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U8197; AAC47041.1; -
DR HSSP; O06124; 2SHD.
DR DictyDb; DD01111; ptpcl.
DR DictyDb; DP07777; ptpcl.
DR InterPro; IPR00387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYHPHTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolyase.
KW ACT SITE.
FT ACT SITE 649 649
FT DOMAIN 460 716
FT DOMAIN 64 71
FT DOMAIN 109 118
FT DOMAIN 137 190
FT DOMAIN 249 257
FT DOMAIN 258 265
FT DOMAIN 289 289
FT DOMAIN 366 371
FT DOMAIN 787 790
FT DOMAIN 834 839
FT DOMAIN 883 892
FT DOMAIN 906 914
FT DOMAIN 943 963
FT DOMAIN 989 989
SQ SEQUENCE 989 AA; 109995 MW; 9371105AF80974AF CRC64;

Query Match 7.7%; Score 107.5; DB 1; Length 989;
Best Local Similarity 19.1%; Pred. No. 1.4;
Matches 45; Conservative 53; Mismatches 81; Indels 57; Gaps 9;

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:59:08 ; Search time 31.9628 Seconds
(Without alignments)
2204.073 Million cell updates/sec

Title: US-09-224-683-61

Perfect score: 1397
Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISMLQEKEREFQEV 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriaph:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	865	61.9	208	11	Q64384
2	509	36.4	123	11	Q61854 mus musculu
3	480	34.4	160	11	Q8C9K1 mus musculu
4	375	26.8	271	13	Q9YGP2 ambystoma m
5	302	21.6	270	13	Q8A7N7 xenopus lae
6	145	10.4	36	6	Q8SPK7 canis famli
7	127	9.1	1697	5	Q81FW4 plasmodium
8	127	9.1	1713	5	Q8MWP2 plasmodium
9	127	9.1	1713	5	Q8MWP2 plasmodium
10	127	9.1	1716	5	Q8MWP2 plasmodium
11	106	7.6	465	16	Q97H56 clostridium
12	105.5	7.6	1498	3	Q86VK6 emericeila
13	105.5	7.6	1498	3	Q9P884 emericeila
14	102	7.3	792	5	Q9BP83 dictyosteli
15	101	7.2	1490	5	Q19545 caenorhabdi
16	100.5	7.2	402	11	Q35444 mus musculu

17	100.5	7.2	647	10	Q8GSC2 oryza sativ
18	100.5	7.2	647	16	Q98PP9 mycoplasma
19	100	7.2	1501	3	Q96VL9 botrytis ci
20	99	7.1	937	10	Q9MAL4 arabidopsis
21	97.5	7.0	1107	3	Q12271 saccharomy
22	97	6.9	253	11	Q8R546 mus musculu
23	97	6.9	1447	16	Q9PQJ8 ureaplasma
24	97	6.9	1566	11	Q9RIL5 mus musculu
25	96.5	6.9	345	15	Q8OEF1 human immun
26	96.5	6.9	373	12	Q8O528 chimpanzee
27	96.5	6.9	475	11	Q9D6C8 mus musculu
28	96.5	6.9	1056	16	Q8RE77 fusobacteri
29	96	6.9	464	16	Q8EQ50 oceanobacti
30	96	6.9	1185	16	Q8XJP0 clostridium
31	96	6.9	3072	12	Q92645 clover yell
32	95.5	6.8	345	15	Q8O528 human immun
33	95.5	6.8	348	15	Q8QED9 human immun
34	95.5	6.8	484	5	Q01626 caenorhabdi
35	95.5	6.8	614	10	Q91Q29 arabidopsis
36	95.5	6.8	683	2	Q50281 mycoplasma
37	95.5	6.8	806	2	Q9L8P7 mycoplasma
38	95.5	6.8	1515	3	Q96VK4 emericeila
39	94.5	6.8	576	11	Q62970 ratius norv
40	94.5	6.8	579	11	Q99KW2 mus musculu
41	94.5	6.8	632	4	Q8NDW9 homo sapien
42	94.5	6.8	722	11	Q8BZT8 mus musculu
43	94	6.7	550	10	Q48935 mentha pipe
44	94	6.7	1896	5	Q8MN73 dictyosteli
45	93.5	6.7	1816	5	Q81095 caenorhabdi

ALIGNMENTS

RESULT 1
Q64384 PRELIMINARY; PRT; 208 AA.
AC Q64384;
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Mast cell growth factor (Fragment).
GN KITL OR MGF OR SL OR KL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
OC
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92330001; PubMed=1378327;
RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
RT "Differential expression and processing of two cell associated forms
of the Kit-ligand: KL-1 and KL-2".
RT Mol. Biol. Cell 3:349-362(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160046; PubMed=1705866;
RA Flanagan J.G., Chan D.C., Leder P.;
RT "Transmembrane form of the Kit ligand growth factor is determined by
RT alternative splicing and is missing in the Sid mutant".
RL Cell 64:1025-1035(1991).
DR EMBL: S40536; AAB22556.2; -;
DR EMBL: M64262; AAB39378.1; -;
DR WGD; MG1:96974; KitL.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
FT NON TER 208
SQ SEQUENCE 208 AA; 23222 MW; C74DD639566EB817 CRC64;

Query Match 61.9%; Score 865; DB 11; Length 208;
Best Local Similarity 82.8%; Pred. No. 5.8e-63;
Matches 169; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKKTOTWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPRKDYMITLKYVPG 60
DB 1 MKKTOTWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPRKDYMITLKYVPG 60
QY 61 MDVLPSCWISSENVVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEVKENS 120
DB 61 MDVLPSCWISSENVVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEVKENS 120
QY 121 KDLKSGFKSPERPLFTPEEFERFENSIDAFKDFVVASSTSDCVSSSTLSPKDSRVST 180
DB 121 KNLKSPKRPETSPFPEEFESIFNNSIDAFKDFVVASSTSDCVSSSTLSPKDSRVST 180
QY 181 KPFLPVAASSLRNDSSSSNRKA 204
DB 181 KPFLPVAASSLRNDSSSSNRKA 204
QY 181 KPFLPVAASSLRNDSSSSNRKA 204
DB 181 KPFLPVAASSLRNDSSSSNRKA 204

RESULT 2
Q61854 PRELIMINARY; PRT; 123 AA.
AC 061854
DB 061854
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Mast cell growth factor.
GN KITL OR MGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RT "Molecular analysis of two new Steel mutations in mice shows a
transversion or an insertion."
RL Mamm. Genome 7:843-846 (1996).
DR EMBL; X95379; CAA64666.1; -.
DR MGD; MGJ:96974; KITL.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
SQ SEQUENCE 123 AA; 13892 MW; A872B4554A85D642 CRC64;

Query Match
Best Local Similarity 36.4%; Score 509; DB 11; Length 123;
Matches 98; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKTOTWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPRKDYMITLKYVPG 60
DB 1 MKKTOTWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPRKDYMITLKYVPG 60
QY 61 MDVLPSCWISSENVVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEVKENS 120
DB 61 MDVLPSCWISSENVVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEVKENS 120
QY 121 K 121
DB 121 K 121

RESULT 3
Q6C9K1 PRELIMINARY; PRT; 160 AA.
AC 06C9K1
DB 06C9K1
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Kit ligand (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; Pubmed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK041961; BAC31113.1; -.
FT NON TER 160
SQ SEQUENCE 160 AA; 17492 MW; B12AC581346AA6D CRC64;

Query Match
Best Local Similarity 34.4%; Score 480; DB 11; Length 160;
Matches 92; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 6 TWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPRKDYMITLKYVPGMDVLP 65
DB 46 TWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPRKDYMITLKYVPGMDVLP 105
QY 66 SHCWISSENVVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEVKENS 119
DB 106 SHCWISSENVVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEVKENS 159

RESULT 4
Q9YGP2 PRELIMINARY; PRT; 271 AA.
AC Q9YGP2
DB Q9YGP2
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Steel factor.
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroides; Ambystomatidae;
OX NCBI_Taxid=8296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99299573; Pubmed=10370116;
RT Parichy D.M., Stigson M., Voss S.R.;
"Genetic analysis of steel and the P-G/M/versican-encoding gene AXPg as
candidates for the white (d) pigmentation mutant in the salamander
RT Ambystoma mexicanum."
RL Dev. Genes Evol. 209:349-356 (1999).
DR EMBL; AF119044; AAD17253.1; -.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
SQ SEQUENCE 271 AA; 30075 MW; 876977ABE7D3EB4 CRC64;

Query Match
Best Local Similarity 26.8%; Score 375; DB 13; Length 271;
Matches 100; Conservative 40; Mismatches 111; Indels 26; Gaps 8;

QY 1 MKKTOTWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPRKDYMITLKYVPG 56
DB 1 MKKTOTWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPRKDYMITLKYVPG 53
QY 57 YVPGMDVLPSCWISSENVVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEVK 116
DB 54 YVPGMDVLPSCWISSENVVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEVK 110
QY 117 -----ENSSKDKKSGFSPERPLFTPEEFERFENSIDAFKDFVVASSTSDCVS-STLSP 171
DB 111 SOLIDNEBFTIDPFYDGE---FVPEKFKYVVTITLLFKAIHKMDSDSTCELPVTFETP 167
QY 172 EKDSRVSTKRPMLPVAASSLRNDSSSSNRKAKNPDDSSLLHMAAALPLPFLSIIIGFA 231
DB 168 LSPDIPVGTKPSAKRFPSSSRKREGIPNKKPSTSG-LALETPPYALISLSLVIGFI 226
QY 232 FGALYWKRPQPSLRRAVE---NIQINEEDNEISMLOE 265

Db 227 IGVCWCMKMRBSGCEPTAPCPVRKKAQASMLNQ 263

RESULT 5

Q8AN7 PRELIMINARY; PRT; 270 AA.

AC Q8AN7; 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DE Stem cell factor.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodidae; Xenopus.
 NC NCB1_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Katada T., Yamamoto T., Kitano T., Abe S., Kinoshita T.;
 RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB084915; BAC23087.1; -
 SQ SEQUENCE 270 AA; 31017 MW; 462435081000B73A CRC64;

Query Match 21.6%; Score 302; DB 13; Length 270;
 Best Local Similarity 29.7%; Pred. No. 8.7e-17;
 Matches 84; Conservative 47; Mismatches 110; Indels 42; Gaps 9;

QY 1 MKKTQWILTCIVYQLLF--NPLVTEGICRNRVTNNKDYTKLVANLPKDYMTLTKY 57
 1 MKKTWIIICINLQFLHCFGRP-----CGNPITDAVNDIPKLVGNIPNDYNNVSV 53
 DB 58 VPGMDVLPSCWISSENVQVLSLTLDLDFSNISELSYSIIDKLVNIVDLVCEVKE 117
 54 VPEKDGLPKHCWLVYMWVETNLDKLSKFEKNTSQ--NVLIIKLSWIFGQIRIOCIQ 110
 QY 118 NSSKDLKSKSPKPEPRFTPEEFPRIFNRSIDAFKQPVVASSESDCVSSTLSPEKDSV 177
 111 NDEMDEPSASLYRVEYKARDFSVYVSTIEVFKINDTEYSRLCI--LPQEEPEFY 166
 DB 178 SVTKPEFL-----PVAASSLRNDSSSNRKAQNPQDSLSHMAALPALFSLI 227
 167 TTEDDFILDSNDLPVPESTRKNSRFDSSARSGETG---TSIQYSTV-LIALACLV 221
 QY 228 IGFAFGAL-YWKRQPSLTRAVENIQINEEDNEISMLOEKERE 269
 222 IGFLGVLCLMK-----FKHRTQTQDNLSAVAVEPRAE 255
 DB

RESULT 6
 Q8SPM7 PRELIMINARY; PRT; 36 AA.

AC Q8SPM7; 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DE Mast cell growth factor (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteheria; Carnivora; Plissipedia; Canidae; Canis.
 NC NCB1_TaxID=9615;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Schmutz S.M., Berryere T.G.;
 RT "MGP sequencing in the dog aids in mapping to CFA15";
 DR EMBL; AY094360; AAM16279.1; -
 DR InterPro; IPR003452; SCF.
 DR Pfam; PF02404; SCF; 1.
 FT NON_TER 1 1
 FT 36 36

SQ SEQUENCE 36 AA; 4004 MW; D96DD4CF5426F594 CRC64;

Query Match 10.4%; Score 145; DB 6; Length 36;
 Best Local Similarity 78.8%; Pred. No. 4.9e-05;
 Matches 26; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 217 AMALPALFSLIIGFAFGALYWKRPQPSLTRAVE 249
 4 SLALPAPFSVIGFAFGALYWKRPQPSLTRIVE 36
 DB

RESULT 7
 Q8IFM4 PRELIMINARY; PRT; 1697 AA.

AC Q8IFM4; 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DE Hypothetical protein.
 GN PFD1150C.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NC NCB1_TaxID=36329;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Hamlin N., Pain A., Berriman B., Hall N., Bowman S., Churcher C.,
 RA Harris B., Harris D., Lawson D., Quail M., Barrell B.;
 RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL035477; CAD49276.1; -
 SQ SEQUENCE 1697 AA; 203378 MW; 02274728866E0B2A CRC64;

Query Match 9.1%; Score 127; DB 5; Length 1697;
 Best Local Similarity 21.1%; Pred. No. 0.17;
 Matches 53; Conservative 52; Mismatches 102; Indels 44; Gaps 11;

QY 31 NRVNNVQDVTKLVAN-----LPRDYMTLKYVGM-DVLPSCWISSENV--Q 76
 1201 KXINNLDKDTIIVINDNNTLOEQRINELONKIKQKNSDVTHNINSQILNTSQ 1260
 QY 77 LSDSLTDLDFKFSNISEG--VSIIIDKLVNIYD-DLVECVKNSKDLKSKSPKPEP 132
 1261 AQNSFFNIPMKQINNDINSKRYNVQKITEIINSYDIN-YNNQNIKDIYQCFKNIQ 1319
 DB 133 RLPTPEEFPRIFNRSIDAFKQPVVASSESDCVSSTLSPEKDSRVSITKPEFLPVAAS 192
 1320 QINTTETQNLHKNINHKYKYESHQITISIV--KRMQNEKIKIQEFNKKI-----QH 1370
 QY 193 LKNDSSSNRKAQNPQDSLSHMAALPAL--FSLIIGFAFGALYWKRPQPSLTRAVE 249
 1371 FKEETQIMINKLIQ--SHIHLHKKLPITQOQILNTIL-----HREQTKNATR 1417
 DB 250 NIQINEEDNEI 260
 1418 SYNNAEENEM 1428
 QY

RESULT 8
 Q8MMP2 PRELIMINARY; PRT; 1711 AA.

AC Q8MMP2; 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DE Reticulocyte binding protein-like protein 4.
 GN RH4.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NC NCB1_TaxID=5833;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Indochina III/CDC;
 MEDLINE=22030722; PubMed=12034462;

RA Kaneke O., Mu J.-B., Tsuboi T., Su X.-Z., Torii M.;
RT "Gene structure and expression of a Plasmodium falci-parum 220-kDa
RT protein homologous to the Plasmodium vivax reticulocyte binding
RL Mol. Biochem. Parasitol. 121:275-278 (2002).
DR EMBL; AF420309; AAM47174.1; -
SQ SEQUENCE 1711 AA; 205236 MW; 2548B64576A02A5B CRC64;

Query Match 9.1%; Score 127; DB 5; Length 1711;
Best Local Similarity 21.1%; Pred. No. 0.17;
Matches 53; Conservative 52; Mismatches 102; Indels 44; Gaps 11;

QY 31 NRVTVNVKDYTKLVAN-----LPKDYMTLKVPYGM-DVLPSCMISEMVV---Q 76
AC Q8MWP1; PRELIMINARY; PRT; 1713 AA.
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DB 1219 HKINNNLKDIHIVINDNNTLQEQNRINYELQNKIKQIKVSDVFTNINVSQQLINVSQ 1278
QY 77 LSDSLDLDDKPSNISGLSN--YSIIDKLVNIYD--DLVECKENSSKDLKSKFSPEP 132
DB 1279 AONSFFNIFMKFONINNDINSKRYVQKITEIINSYDIIN-YKNKNIKDIYQOFKNIQ 1337
QY 133 RLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVTKPMLPVAASS 192
DB 1338 QLTETETQLNHIKQININHFYFESHOTISIV--KNNQNEKTKIQEENKTI-----QH 1388
QY 193 LRNDSSSNRRKAKNPBGSSSLHWAAMALPAL---FSLIIGFAGALYWKRPQSLTRAWE 249
DB 1389 FKEETQIMINKLIQ---SHIHLHKMKLPIRQOQLNTL-----HNEQTQKNAIR 1435
QY 250 NIQINEEDNEI 260
DB 1436 SYNMBEENEM 1446

RESULT 9

ID Q8MWP1 PRELIMINARY; PRT; 1713 AA.
AC Q8MWP1;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DB 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Reticulocyte binding protein-like protein 4.
GN RH4.
OS Plasmodium falci-parum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN RP SEQUENCE FROM N.A.
RC STRAIN=Honduas I/CDC;
RX MEDLINE=22030722; PubMed=12034462;
RA Kaneke O., Mu J.-B., Tsuboi T., Su X.-Z., Torii M.;
RT "Gene structure and expression of a Plasmodium falci-parum 220-kDa
RT protein homologous to the Plasmodium vivax reticulocyte binding
RT protein."
RL Mol. Biochem. Parasitol. 121:275-278 (2002).
DR EMBL; AF420310; AAM47175.1; -
SQ SEQUENCE 1713 AA; 205500 MW; AE975734989F495D CRC64;

Query Match 9.1%; Score 127; DB 5; Length 1713;
Best Local Similarity 21.1%; Pred. No. 0.18;
Matches 53; Conservative 52; Mismatches 102; Indels 44; Gaps 11;

QY 31 NRVTVNVKDYTKLVAN-----LPKDYMTLKVPYGM-DVLPSCMISEMVV---Q 76
DB 1223 HKINNNLKDIHIVINDNNTLQEQNRINYELQNKIKQIKVSDVFTNINVSQQLINVSQ 1282
QY 77 LSDSLDLDDKPSNISGLSN--YSIIDKLVNIYD--DLVECKENSSKDLKSKFSPEP 132
DB 1283 AONSFFNIFMKFONINNDINSKRYVQKITEIINSYDIIN-YKNKNIKDIYQOFKNIQ 1341
QY 133 RLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVTKPMLPVAASS 192
DB 1342 QLTETETQLNHIKQININHFYFESHOTISIV--KNNQNEKTKIQEENKTI-----QH 1392

QY 193 LRNDSSSNRRKAKNPBGSSSLHWAAMALPAL---FSLIIGFAGALYWKRPQSLTRAWE 249
DB 1393 FKEETQIMINKLIQ---SHIHLHKMKLPIRQOQLNTL-----HNEQTQKNAIR 1439
QY 250 NIQINEEDNEI 260
DB 1440 SYNMBEENEM 1450

RESULT 10

ID Q8MWH2 PRELIMINARY; PRT; 1716 AA.
AC Q8MWH2;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DB 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Reticulocyte binding protein homolog 4.
GN RH4.
OS Plasmodium falci-parum (isolate NF54).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5843;
RN RP SEQUENCE FROM N.A.
RC MEDLINE=22030722; PubMed=12034462;
RA Kaneke O., Mu J.-B., Tsuboi T., Su X.-Z., Torii M.;
RT "Gene structure and expression of a Plasmodium falci-parum 220-kDa
RT protein homologous to the Plasmodium vivax reticulocyte binding
RT protein."
RL Mol. Biochem. Parasitol. 121:275-278 (2002).
DR EMBL; AF432854; AAM47192.1; -
SQ SEQUENCE 1716 AA; 205846 MW; 2A3DAC35B6FEF226 CRC64;

Query Match 9.1%; Score 127; DB 5; Length 1716;
Best Local Similarity 21.1%; Pred. No. 0.18;
Matches 53; Conservative 52; Mismatches 102; Indels 44; Gaps 11;

QY 31 NRVTVNVKDYTKLVAN-----LPKDYMTLKVPYGM-DVLPSCMISEMVV---Q 76
DB 1220 HKINNNLKDIHIVINDNNTLQEQNRINYELQNKIKQIKVSDVFTNINVSQQLINVSQ 1279
QY 77 LSDSLDLDDKPSNISGLSN--YSIIDKLVNIYD--DLVECKENSSKDLKSKFSPEP 132
DB 1280 AONSFFNIFMKFONINNDINSKRYVQKITEIINSYDIIN-YKNKNIKDIYQOFKNIQ 1338
QY 133 RLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVTKPMLPVAASS 192
DB 1339 QLTETETQLNHIKQININHFYFESHOTISIV--KNNQNEKTKIQEENKTI-----QH 1389
QY 193 LRNDSSSNRRKAKNPBGSSSLHWAAMALPAL---FSLIIGFAGALYWKRPQSLTRAWE 249
DB 1390 FKEETQIMINKLIQ---SHIHLHKMKLPIRQOQLNTL-----HNEQTQKNAIR 1436
QY 250 NIQINEEDNEI 260
DB 1437 SYNMBEENEM 1447

RESULT 11

ID Q97H56 PRELIMINARY; PRT; 465 AA.
AC Q97H56;
DT 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DB 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Flagellar hook-length control protein flik.
GN CAC2157.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VGM B-1787;

RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.,
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum".
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007716; AAK80115.1; -.
KM Complete proteome.
SQ SEQUENCE 465 AA; 51441 MW; 076B343B7D0A678B CRC64;

Query Match 7.6%; Score 106; DB 16; Length 465;
Best Local Similarity 27.5%; Pred. No. 1.8;
Matches 52; Conservative 35; Mismatches 76; Indels 26; Gaps 8;

QY 38 KDVTYLVANIPKQYMTLTKVY---PGMDVLPSCWISSEMVOLSLDLDKFSNISE 93
DB 101 KEIKTKIVSKLNGDLELDIKDKGKTDMSLIOQ---MLEMLIKNGACSDDELKAKMKA 157
QY 94 GLANSYSLIDLVNIVDDVLCVCKENSKDLKSKSPKS-----PPRLFTPEEPRFRINRSI 148
DB 158 GISD-EVQDKLMKVMHDIKELKNNSGKDLTKTLDLSLSTGNSSLAEKSLIRDI--1 213
QY 149 DAFKDFVASETSDCVSVSTLSPEKDSRVSVTKPFMLPYAASSLRN-----DSSSNRK 203
DB 214 DSLKKKL---NGSDALNSSSKFDNDFEDKGTIDQAGSSVLSGKNTKASYDSDETNEQ 270
QY 204 AKNPDDSS 212
DB 271 AKS--GDSS 277

RESULT 12

Q96VK6 PRELIMINARY; PRT; 1498 AA.
AC Q96VK6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE ABC transporter protein.
GN ATRE.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
RN NCBI_TaxID=162425;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG096;
RA Andrade A.C., Braam C., Haas H., De Waard M.A.;
RT "ABC transporters and resistance to azole fungicides in the ima
RT mutants of Aspergillus nidulans".
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL: AJ309280; CAC42216.1; -.
DR InterPro: IPR003593; AAA ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR000847; HTH_LYSR.
DR InterPro: IPR001063; Ribosomal_L22.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transporter; 2.
DR SMART: SM00382; AAA; 2.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
DR PROSITE: PS00464; RIBOSOMAL_L22; 1.
KM ATP-binding; Transport.
SQ SEQUENCE 1498 AA; 167675 MW; EBE9FF3F46110FEB CRC64;

Query Match 7.6%; Score 105.5; DB 3; Length 1498;
Best Local Similarity 20.3%; Pred. No. 8.5;
Matches 59; Conservative 41; Mismatches 108; Indels 83; Gaps 10;
QY 17 LLENPLVKT-----EGICRNRVTNNVVDVTKLVANIPKQYMTLTK-----YVPG----- 60

DB 263 LMFSAALAPRRRLBEGVSRKQYAEHMRDY--VMAMLGSHITINTVGNDFIRGVSGGERK 320
QY 61 -----MDVLPSCWISB-----MVVQLSDSLTD 83
DB 321 RVSIAEATLSQAPLQCDWNSRTRGLDSANALBFCKNIALMSKYTGSTACVAIYQASQAYD 380
QY 84 LLDKPSNISSEGLSNY--SLIDLVNIVDDVLCVCKENSKDLKSKSPKPEPLF----- 135
DB 381 VDKVTYLVLEGQIYFGNTKDAKKFFVDMGECPEPRQTTADPLTSLTSPAERLVAPGEG 440
QY 136 -----TPPEEPRFRINSDAFK-----DFVASETSDCVSVSTLSPEKDSRVSVTK 181
DB 441 RVPCPTPEFAAMAKRSERAKLMATIEYERQYPIGSPSYAFVADARAKMQ-SKRQRVNS 499
QY 182 PMLPFPVAASSLRNDSNRSKAKKPPDDSSIHMAAMLPAFLSLITGFAF 232
DB 500 PYTI-----SIQOVSLCVRGFORLRDPSLTSTSLIGNFMWALLIGSVF 545

RESULT 13

Q9P884 PRELIMINARY; PRT; 1498 AA.
AC Q9P884;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE ABC transporter protein.
GN ATRE.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
RN NCBI_TaxID=162425;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG096;
RA Andrade A.C., Van Nistelrooy J.G.M., Haas H., De Waard M.A.;
RT "ABC transporters and resistance to azole fungicides in the ima
RT mutants of Aspergillus nidulans".
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL: AJ276241; CAB76823.1; -.
DR InterPro: IPR003593; AAA ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR000847; HTH_LYSR.
DR InterPro: IPR001063; Ribosomal_L22.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transporter; 2.
DR SMART: SM00382; AAA; 2.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
DR PROSITE: PS00464; RIBOSOMAL_L22; 1.
KM ATP-binding; Transport.
SQ SEQUENCE 1498 AA; 167706 MW; AABDEA3FFD1ABFEB CRC64;

Query Match 7.6%; Score 105.5; DB 3; Length 1498;
Best Local Similarity 20.3%; Pred. No. 8.5;
Matches 59; Conservative 41; Mismatches 108; Indels 83; Gaps 10;

QY 17 LLENPLVKT-----EGICRNRVTNNVVDVTKLVANIPKQYMTLTK-----YVPG----- 60
DB 263 LMFSAALAPRRRLBEGVSRKQYAEHMRDY--VMAMLGSHITINTVGNDFIRGVSGGERK 320
QY 61 -----MDVLPSCWISB-----MVVQLSDSLTD 83
DB 321 RVSIAEATLSQAPLQCDWNSRTRGLDSANALBFCKNIALMSKYTGSTACVAIYQASQAYD 380
QY 84 LLDKPSNISSEGLSNY--SLIDLVNIVDDVLCVCKENSKDLKSKSPKPEPLF----- 135
DB 381 VDKVTYLVLEGQIYFGNTKDAKKFFVDMGECPEPRQTTADPLTSLTSPAERLVAPGEG 440
QY 136 -----TPPEEPRFRINSDAFK-----DFVASETSDCVSVSTLSPEKDSRVSVTK 181

Db 441 RVCCTPDEFAAANKREBEERAKLMALIEEYERQYPIGGSSYDAFVDARAKMG-SKGRQVNS 499

Qy 182 PFMLPVAABSLANDSSSNRKAKNPGRGSSLHMAAMLPALFSLITIGFAT 232

Db 500 PYTL-----SIQQQVSLCVVRCGRQARSGPFSLITTSLSLGNPFMALITISVF 545

RESULT 14

ID	G9BPV3;	PRELIMINARY;	PRT;	792 AA.
AC	G9BPV3;			
DT	01-JUN-2001 (TrEMBLrel. 17, Created)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)			
DE	Dd kinesin-related protein K2.			
GN	DDK2.			
OS	Dictyostelium discoideum (Slime mold).			
OC	Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.			
OX	NCBI_TaxID=44689;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Ax2;			
RA	Iwai S., Suyama E., Adachi H., Sutoh K.;			
RT	"Characterization of Kinesin-related Protein K2 from Dictyostelium			
RL	discoideum";			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			

RP SEQUENCE FROM N.A.
RC STRAIN=Ax2;
RX MEDLINE=98359834; PubMed=9693369;
RA De hostos E.L., Mc Caffrey G., Sugang R., Pierce D.W., Vale R.D.
RT "A Developmentally Regulated Kinesin-related Motor Protein From
R1 Dictyostelium discoidium.";
RL Mol. Biol. Cell 9:2093-2106(1998).

DR HSSP_P17119; 3KAR. kinesin_motor.
DR InterPro; IPR001752. kinesin_1.
DR Pfam; PF00225. kinesin_1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM0129; Kisc_1.
DR PROSITE; PS0067. KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Coiled coil; Microtubules; Motor protein
SQ SEQUENCE 792 AA; 89360 MW; 023EA4F995E76F CRC64

Query Match	7.38; Score 102; DB 5; Length 792;
-------------	------------------------------------

Matches 59; Conservative 60; Mismatches 111; Indels 70; Gaps 12;

QY 13 YLQLLFNPLVKTEGI-----CRNRVTNNVKDVTKLVANLPKDY-----MITLKVYPGMD 62

D6 59 YH0PLLTNTB1KLEDISSSSNNNPLKNSINNVSQISSLNSSHHSRALMQKNNPTTN 118

```
63 VLP$HCWISEMVQLSDSLDLDR-----SNISGGLSNYSIDLKLVNIDDLVECV 115
```

[illegible][illegible][illegible]

```

      : :: : || ::
225 NDNNNNTS-----SSCSNNSGEDI OOHAI YEBMNYKTDOETOTVBCN 268
      : :: : || ::

```

230 --FAEGAI.YWKKRPSI.TRAVENTOTN---EEDNE-----TSMI.OEKERBEFOE 372

Db 269 LOSQFDNISQLKPPRLSLISIODIKTRLDFEENKKEVEKIKLEKNVLOSLKEKEKELME 328

RESULT 15

ID	Q19545	PRELIMINARY;	PRT;	1490	AA.
AC	Q19545;				

DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 168.5 kDa protein.

05 *Caenorhabditis elegans*.
0C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae.
0C Rhabditidae; Pelodierinae; Caenorhabditis.
0X NCBI_TaxID=6239;
/s/1

RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;

RT Investigating biology. The C. elegans Sequencing Consortium. *Science* 282:2012-2018 (1998).
 RL [2]
 RN SEQUENCE FROM N. A.
 RP *omb-22.2* (n110)
 RC

RA Fulton L.;
RT "the sequence of *C. elegans* cosmid F18C5.",
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]

RC STRAIN=Briseol N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBD databases.

DR wormPep; F18C5.3; C602652.
KM Hypothetical protein.
SQ SEQUENCE 1490 AA; 168480 MW; 89FF7AD689A3E668 CRC64;

Best Local Similarity 23.9%; Pred. No. 20;
 Matches 50; Consensus 70; Mismatch 00; Indel 00; Consensus 00

30 NPI.VKTEGICBNBYTNNVKDYTKI.YANI.BKDYMITI.KYVBCMDYI.BSHCWISEMAYOI.S

Db 732 NGAYKAE--CPRAKGNBAPEMOHLGRIVSPAGIOMTLAFRDVNEH--PSAKAYO--

QY 80 SLTDLDFSNISEGLSNYSIID-----KLVNIVDDLVECVKENSSKDLKKSFK

Db 785 RVSDLISKFAG---GLKDNESLDHSQLGYIFKSLTSDIQKLELVETKNGQKDEKQKGR

130 PEPRLETFEEFRI--FNRSIDAFKDFVASETSDCVSSTLSPEK-----DSRVSVTIK

Db 842 PESCLLPAPQIRIGAMSKVIRSRDHVFA-EFFVLLFSSLKEKKFDLSDDSMVSRLN

QY 183 FM-----LPVVAASSLR-----NDSSSSNRK

DD 301 FVNIIDCFDFAIENISCSMKALSSMI QMQLFAIHSNSQKVS DI EF ILSDI331GDA

—

Search completed: February 5, 2004, 15:07:29

PA (AMGE-) AMGEN INC.
 XX Zeebo KM, Suggs SV, Bosselman RA, Martin FH;
 PI WPI, 1991-119233/17.
 XX N-PSDB; AAQ11543.
 DR
 PT New naturally-occurring polypeptide stem cell factor analogues -
 PT have haematopoietic biological activity of stem cell factor and
 PT are used to treat eg leucopenia, AIDS, nerve damage and
 PT infertility
 XX
 XX Disclosure; Fig 44; 127pp; English.
 XX
 CC The SCF has the ability to stimulate growth of primitive
 CC progenitors including early hematopoietic progenitor cells and non-
 CC hematopoietic stem cells such as neural stem cells and primordial
 CC germ stem cells. The product may be used in a pharmaceutical
 CC compen. for treating, in a mammal, leucopenia, thrombocytopenia,
 CC anaemia, AIDS, neoplasia, nerve damage, infertility and
 CC intestinal damage.
 CC See also AAR11708, AAQ11509-Q11543.
 XX
 SQ Sequence 245 AA;
 Query Match 100.0%; Score 1262; DB 12; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.5e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVADVTKLVANLPKDYMITLKYPVG 60
 DB 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVADVTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIDKLVINIVDDLVECKENSS 120
 DB 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIDKLVINIVDDLVECKENSS 120
 QY 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPEKAKNPP 180
 DB 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPEKAKNPP 180
 QY 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPEKAKNPP 180
 DB 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPEKAKNPP 180
 QY 181 GDSLSHMAAMALPALFSLITGFAGALYMKKROPSLTRAVENTIQINEEDNEISMLQEKER 240
 DB 181 GDSLSHMAAMALPALFSLITGFAGALYMKKROPSLTRAVENTIQINEEDNEISMLQEKER 240
 QY 241 EFOEV 245
 DB 241 EFOEV 245
 QY 241 EFOEV 245
 DB 241 EFOEV 245
 RESULT 2
 AAR83979
 ID AAR83979 standard; Protein; 245 AA.
 XX
 XX AAR83979;
 AC
 XX
 DT 25-MAR-2003 (updated)
 DT 15-MAY-1996 (first entry)
 XX
 DE Human stem cell factor derived from 5637 bladder carcinoma cell line.
 XX
 XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
 KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
 KW transplant; neoplasia; myelosuppression; bone marrow; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT Protein /label= sig_peptide
 FT 26..245
 FT /label= mat_SCF
 XX

PN EP676470-A1.
 XX
 PD 11-OCT-1995.
 XX
 XX 04-OCT-1990; 95EP-0105391.
 PF
 XX 01-OCT-1990; 90US-0589701.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90WO-0505548.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 PI Bosselman RA, Martin FH, Suggs SV, Zeebo KM;
 XX
 XX WPI, 1995-346090/45.
 DR N-PSDB; AAT04891.
 XX
 PT New stem cell factor polypeptide(s) - for stimulating the growth of
 PT primitive progenitor cells, esp. for treating disorders involving
 PT blood cells
 XX
 XX Claim 9; Fig 44; 127pp; English.
 XX
 PS AAR83979 is a human stem cell factor (SCF) derived from the 5637 bladder
 CC carcinoma cell line. Non-naturally occurring SCF and C-terminally
 CC truncated polypeptides, having amino acid sequences sufficiently
 CC duplicative of naturally occurring SCF, stimulate growth of primitive
 CC progenitors such as haematopoietic progenitor cells, neural stem
 CC cells and primordial germ stem cells. The peptides can be used in a
 CC composition for treating leucopenia, anaemia or thrombocytopenia,
 CC for enhancing engraftment of bone marrow during transplantation or
 CC for bone marrow recovery after chemotherapy or radiation-induced bone
 CC marrow aplasia or myelosuppression. They can also be used for
 CC treating neoplasia, nerve damage, infertility, intestinal damage or
 CC myeloproliferative disorders. Antibodies may be raised against the
 CC peptides for use in detection or neutralisation of SCF in serum. SCF
 CC may be useful for the treatment of AIDS and severe combined
 CC immunodeficiency (SCID) states alone or in combination with other
 CC factors such as IL-7.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 SQ Sequence 245 AA;
 Query Match 100.0%; Score 1262; DB 16; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.5e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVADVTKLVANLPKDYMITLKYPVG 60
 DB 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVADVTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIDKLVINIVDDLVECKENSS 120
 DB 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIDKLVINIVDDLVECKENSS 120
 QY 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPEKAKNPP 180
 DB 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPEKAKNPP 180
 QY 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPEKAKNPP 180
 DB 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPEKAKNPP 180
 QY 181 GDSLSHMAAMALPALFSLITGFAGALYMKKROPSLTRAVENTIQINEEDNEISMLQEKER 240
 DB 181 GDSLSHMAAMALPALFSLITGFAGALYMKKROPSLTRAVENTIQINEEDNEISMLQEKER 240
 QY 241 EFOEV 245
 DB 241 EFOEV 245
 QY 241 EFOEV 245
 DB 241 EFOEV 245
 RESULT 3
 AAU05267
 ID AAU05267 standard; Protein; 245 AA.

```

XX AC AAU05267;
XX DT 24-OCT-2001 (first entry)
XX DE Human SCF protein isolated from the 5637 bladder carcinoma cell line.
XX KM Human, stem cell factor; SCF; haematopoietic progenitor cell; AIDS;
XX KM blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
XX KM hypopigmentation disorder; viral disorder; 5637 bladder carcinoma.
XX OS Homo sapiens.
XX FH Key
XX FT Protein 1..25
XX FT /label= Signal_peptide
XX FT Protein 26..245
XX FT /label= Mature_SCF
XX PN US6248319-B1.
XX PD 19-JUN-2001.
XX PF 24-MAY-1995; 95US-0449653.
XX PR 10-APR-1991; 91US-0684535.
XX PR 25-NOV-1992; 92US-0982255.
XX PR 16-OCT-1989; 89US-0422383.
XX PR 11-JUN-1990; 90US-0537198.
XX PR 24-AUG-1990; 90US-0573616.
XX PR 01-OCT-1990; 90US-0589701.
XX PR 21-DEC-1993; 93US-0172329.
XX PA (ZSEB/) ZSEBO K M.
XX PA (BOSS/) BOSSSELMAN R A.
XX PA (SUGS/) SUGGS S V.
XX PA (MART/) MARTIN F H.
XX PI Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;
XX WP1; 2001-407312/43.
XX DR N-PSDB; AA510462.
XX PT Increasing the number of early haematopoietic progenitor cells in the
XX PT peripheral blood useful for the treatment of blood disorders including
XX PT Hodgkin's disease comprises the administration of human stem cell
XX PT factor -
XX PS Example 3; Fig 44; 210pp; English.
XX CC The present sequence represents human stem cell factor (SCF). The cDNA
XX CC encoding this sequence is isolated from the 5637 bladder carcinoma cell
XX CC line. The sequence is described in an invention relating to novel stem
XX CC cell factors, the polynucleotides encoding them and methods for
XX CC producing the stem cell factors. The methods involve increasing the
XX CC number of early haematopoietic progenitor cells in human peripheral
XX CC blood by administering a haematopoietically effective human stem cell
XX CC factor polypeptide. The methods are useful for the treatment of blood
XX CC disorders, including myelofibrosis, myelocleorosis, osteopetrosis,
XX CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
XX CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
XX CC anaemia, malaria, vitamin B12 and folic acid deficiency,
XX CC hypopigmentation disorders i.e. piebaldism and viral induced disorders,
XX CC including AIDS.
XX SQ Sequence 245 AA;
XX
XX Query Match 100.0%; Score 1262; DB 22; Length 245;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-121;
XX Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MKKTQWILTCIYQLLEFNPVTEGICRNRVTNNKDVTKLVANLPKDYMITLKVP 60
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

```

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DB 1 MKKTQWILTCIYQLLEFNPVTEGICRNRVTNNKDVTKLVANLPKDYMITLKVP 60
QY 61 MDVLPSCWISSEMVQSDSLTDLDFKFSNISEGSSNYSIIDKLVNIYDVLCEKENS 120
DB 61 MDVLPSCWISSEMVQSDSLTDLDFKFSNISEGSSNYSIIDKLVNIYDVLCEKENS 120
QY 121 KDLKKSFKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASFTSDCVVSTLSPKGRKNPP 180
DB 121 KDLKKSFKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASFTSDCVVSTLSPKGRKNPP 180
QY 181 GSSSLHMAAMALPALPSLITGPAFGALYWKRPQPSLTRAVENTIQINEEDNEISMLOEKER 240
DB 181 GSSSLHMAAMALPALPSLITGPAFGALYWKRPQPSLTRAVENTIQINEEDNEISMLOEKER 240
QY 241 EFOEV 245
DB 241 EFOEV 245

RESULT 4
AAB98368
ID AAB98368 standard; Protein; 245 AA.
XX AAB98368;
XX AC AAB98368;
XX DT 21-AUG-2001 (first entry)
XX DE Human SCF protein sequence SEQ ID NO:63.
XX KM Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
XX KM gene therapy.
XX OS Homo sapiens.
XX PN US6207454-B1.
XX PD 27-MAR-2001.
XX PF 31-DEC-1998; 98US-0224681.
XX PR 21-DEC-1993; 93US-0172329.
XX PR 24-MAY-1995; 95US-0449653.
XX PR 12-JUN-1998; 98US-0005893.
XX PR 25-NOV-1992; 92US-0982255.
XX PR 16-OCT-1989; 89US-0422383.
XX PR 11-JUN-1990; 90US-0537198.
XX PR 24-AUG-1990; 90US-0573616.
XX PR 01-OCT-1990; 90US-0589701.
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;
XX WP1; 2001-36062/38.
XX DR N-PSDB; AA41345.
XX PT Enhancing efficiency of transfer of polynucleotide into a target
XX PT mammalian cell in vitro, involves exposing cell that expresses a stem
XX PT cell factor receptor to stem cell factor, and introducing
XX PT polynucleotide into cell in vitro -
XX PS Claim 18; Fig 44; 210pp; English.
XX CC The present invention describes a method for enhancing (E) the
XX CC efficiency of transfer of a polynucleotide (I) into a target mammalian
XX CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
XX CC factor (SCF) receptor to a biologically active SCF, its analogue or
XX CC fragment, which induces cell proliferation, and introducing (I) to (II)
XX CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)
XX CC into the cell. The method is useful for enhancing the efficiency of the
XX CC transfer of a polynucleotide into a target mammalian cell in vitro.
XX CC The method is useful in gene therapy techniques. AA41301 to AA41364
XX CC and AAB98351 to AAB98390 represent sequences used in the exemplification

```

CC of the present invention.

XX Sequence 245 AA;

Query Match 100.0%; Score 1262; DB 22; Length 245;

Best Local Similarity 100.0%; Pred. No. 1.5e-121;

Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MKKTQWTLTCTIYQLLFNPLVKTGICRNRVTNNVQDVKLVANLPKDYMTLKYVPG 60
   |||||
DB 1 MKKTQWTLTCTIYQLLFNPLVKTGICRNRVTNNVQDVKLVANLPKDYMTLKYVPG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLKPSNISSEGSNYSIIDKLVNIYDVLVECKENS 120
   |||||
DB 61 MDVLPSCWISSEWVQVSDSLTDLKPSNISSEGSNYSIIDKLVNIYDVLVECKENS 120
QY 121 KDLKSKFSPPEPLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNPP 180
   |||||
DB 121 KDLKSKFSPPEPLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNPP 180
QY 181 GDSSLHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
   |||||
DB 181 GDSSLHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
QY 241 EFOEV 245
   |||||
DB 241 EFOEV 245

```

RESULT 5

AAU02461 standard; Protein; 245 AA.

XX AC AAU02461;

XX DT 29-AUG-2001 (first entry)

XX DE Human SCF protein isolated from the 5637 bladder carcinoma cell line.

XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;

XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

XX KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;

XX KW 5637 bladder carcinoma.

XX OS Homo sapiens.

XX FH Key

XX FT Protein

XX FT Protein

XX FT Protein

XX FT Protein

XX FT Protein

XX FT Protein

XX FT Protein

XX FT Protein

XX FT Protein

XX FT Protein

XX FT Protein

XX FT Protein

XX FT Protein

XX FT Protein

XX Novel nucleic acids encoding stem cell factor useful for treating
 PT disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
 XX disease, kala azar, anaemia and septicemia -
 XX Example 5; Fig 44A-44C; 209pp; English.

CC The present sequence representing human SCF (stem cell factor)
 CC protein is isolated from the 5637 bladder carcinoma cell line. The
 CC present invention relates to novel stem cell factors
 CC (AAU02453-AAU02458, AAU02460) and the polynucleotides encoding them.
 CC SCF stimulate primitive progenitor cells including early haematopoietic
 CC progenitor cells. The invention also describes SCF peptides
 CC (AAU02462-AAU02481) and the oligonucleotides (AAS04081-AAS04117) used
 CC in the isolation of human and rat SCF sequences. The polynucleotide
 CC encoding SCF is useful for producing SCF and useful in gene therapy.
 CC It is useful for treating disorders involving blood cells such as
 CC myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 CC Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive
 CC splenomegaly, kala azar, sarcoidosis, military tuberculosis, disseminated
 CC fungus disease, fulminating septicemia, malaria, vitamin B12 and folic
 CC acid deficiency, pyridoxine deficiency, and hypopigmentation disorders
 CC such as prebaldism and vitiligo.

XX SQ Sequence 245 AA;

Query Match 100.0%; Score 1262; DB 22; Length 245;

Best Local Similarity 100.0%; Pred. No. 1.5e-121;

Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MKKTQWTLTCTIYQLLFNPLVKTGICRNRVTNNVQDVKLVANLPKDYMTLKYVPG 60
   |||||
DB 1 MKKTQWTLTCTIYQLLFNPLVKTGICRNRVTNNVQDVKLVANLPKDYMTLKYVPG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLKPSNISSEGSNYSIIDKLVNIYDVLVECKENS 120
   |||||
DB 61 MDVLPSCWISSEWVQVSDSLTDLKPSNISSEGSNYSIIDKLVNIYDVLVECKENS 120
QY 121 KDLKSKFSPPEPLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNPP 180
   |||||
DB 121 KDLKSKFSPPEPLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNPP 180
QY 181 GDSSLHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
   |||||
DB 181 GDSSLHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
QY 241 EFOEV 245
   |||||
DB 241 EFOEV 245

```

RESULT 6

AAU02767 standard; Protein; 245 AA.

XX AC AAU02767;

XX DT 29-AUG-2001 (first entry)

XX DE Human SCF protein isolated from the 5637 bladder carcinoma cell line.

XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;

XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

XX KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;

XX KW 5637 bladder carcinoma.

XX OS Homo sapiens.

XX FH Key

XX FT Protein

XX FT Protein

XX FT Protein

```

XX  US6218148-B1.
PN  17-APR-2001.
XX  21-DEC-1993; 93US-0172329.
XX  25-NOV-1992; 92US-0982255.
PR  16-OCT-1989; 89US-0422383.
PR  11-UTN-1990; 90US-0537198.
PR  24-AUG-1990; 90US-0573616.
XX  01-OCT-1990; 90US-0589701.
XX  (AMGE-) AMGEN INC.
PI  Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
DR  WPI; 2001-281051/29.
XX  N-PSDB; AAS04225.
XX  Isolated DNA sequence, encoding polypeptide product useful for
PT  stimulating growth of early haematopoietic progenitor cells -
XX  Example 5; Fig 44A-44C; 167pp; English.
XX  The present sequence representing human SCF (stem cell factor)
CC  protein is isolated from the 5637 bladder carcinoma cell line. The
CC  present invention relates to novel stem cell factors
CC  (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides
CC  encoding them. SCF stimulate primitive progenitor cells including early
CC  haematopoietic progenitor cells. The invention also describes SCF
CC  peptides (AAU02777-AAU02794) and the oligonucleotides
CC  (AAS04182-AAS04218) used in the isolation of human and rat SCF
CC  sequences. The polynucleotide encoding SCF is useful for producing
CC  SCF and useful in gene therapy. It is useful for treating disorders
CC  involving blood cells such as myelofibrosis, metastatic carcinoma,
CC  acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
CC  Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
CC  sarcoidosis, military tuberculosis, disseminated fungus disease,
CC  fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
CC  pyridoxine deficiency, and hypopigmentation disorders such as
CC  piebaldism and vitiligo.
XX  Sequence 245 AA;
SQ
Query Match 100.0%; Score 1262; DB 22; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.5e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWMLTCTIYQLLEFNPVKTEGICRNVTNNVKDVTXVANLPKDYMITLKYVPG 60
DB 1 MKKTQWMLTCTIYQLLEFNPVKTEGICRNVTNNVKDVTXVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSENVQVSDSLTDLDFKSNISBGLSNYSIIDKLVIIVDLVCEKENS 120
DB 61 MDVLPSCWISSENVQVSDSLTDLDFKSNISBGLSNYSIIDKLVIIVDLVCEKENS 120
QY 121 KDIKKSPKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKGAKNPP 180
DB 121 KDIKKSPKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKGAKNPP 180
QY 181 GDSLSLHMAAALPALPSLIIIGFAFAGALYMKRQPSLTRAVENTQINEEDNEISMLQEKER 240
DB 181 GDSLSLHMAAALPALPSLIIIGFAFAGALYMKRQPSLTRAVENTQINEEDNEISMLQEKER 240
QY 241 EFOEV 245
DB 241 EFOEV 245

```

```

XX  AAB73568;
AC  07-AUG-2001 (first entry)
XX  Human SCF protein isolated from the 5637 bladder carcinoma cell line.
DT  Human; stem cell factor; SCF; early haematopoietic progenitor cell;
DE  blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX  anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
XX  5637 bladder carcinoma.
XX  Homo sapiens.
OS  Key Location/Qualifiers
XX  FT Protein 1..25
XX  FT Protein /label= Signal_peptide
XX  FT Protein 26..245
XX  FT Protein /label= Mature_SCF
XX  US6204363-B1.
XX  20-MAR-2001.
XX  25-NOV-1992; 92US-0982255.
XX  10-APR-1991; 91US-0684535.
XX  16-OCT-1989; 89US-0422383.
PR  11-UTN-1990; 90US-0537198.
PR  24-AUG-1990; 90US-0573616.
PR  01-OCT-1990; 90US-0589701.
XX  (AMGE-) AMGEN INC.
XX  Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI  WPI; 2001-256683/26.
XX  N-PSDB; AAB73568.
XX  New stem cell factor polypeptides and their analogs which stimulate
PT  growth of early haematopoietic progenitors, useful for treating aplastic
PT  anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT  disease -
XX  Claim 10; Fig 44A-44C; 166pp; English.
XX  The present sequence representing human SCF (stem cell factor)
XX  protein is isolated from the 5637 bladder carcinoma cell line. The
XX  present invention relates to novel stem cell factors
XX  (AAB73561-AAB73568, AAB73571-AAB73576) and the polynucleotides
XX  encoding them. SCF stimulate primitive progenitor cells including early
XX  haematopoietic progenitor cells. The invention also describes SCF
XX  peptides (AAB73578-AAB73597) and the oligonucleotides
XX  (AAH23859-AAH23895) used in the isolation of human and rat SCF
XX  sequences. The polynucleotide encoding SCF is useful for producing
XX  SCF and useful in gene therapy. It is useful for treating disorders
XX  involving blood cells such as myelofibrosis, metastatic carcinoma,
XX  acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX  Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
XX  sarcoidosis, military tuberculosis, disseminated fungus disease,
XX  fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX  pyridoxine deficiency, and hypopigmentation disorders such as
XX  piebaldism and vitiligo.
SQ
Sequence 245 AA;
SQ
Query Match 100.0%; Score 1262; DB 22; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.5e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWMLTCTIYQLLEFNPVKTEGICRNVTNNVKDVTXVANLPKDYMITLKYVPG 60
DB 1 MKKTQWMLTCTIYQLLEFNPVKTEGICRNVTNNVKDVTXVANLPKDYMITLKYVPG 60

```

RESULT 7
AAB73568
ID AAB73568 standard; Protein; 245 AA.

QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDKLVNIYVDIVCEVKENSS 120
| | | | |
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDKLVNIYVDIVCEVKENSS 120
| | | | |
QY 121 KDLKKSFKSPERPLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGRKNPP 180
| | | | |
DB 121 KDLKKSFKSPERPLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGRKNPP 180
| | | | |
QY 181 GDSLSHMAAMALPALFSLIIGFAGALYWKGRPSLTRAVENIQINEEDNEISMLQEKER 240
| | | | |
DB 181 GDSLSHMAAMALPALFSLIIGFAGALYWKGRPSLTRAVENIQINEEDNEISMLQEKER 240
| | | | |
QY 241 EFOEV 245
| | | | |
DB 241 EFOEV 245
| | | | |
RESULT 8
AAB96953
ID AAB96953 standard; Protein; 245 AA.
XX
AC AAB96953;
XX
DT 13-JUL-2001 (first entry)
XX
DE Human stem cell factor SEQ ID NO: 63.
XX
XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW gene therapy; hematopoietic disorder; aplastic anaemia; leukaemia;
KW neurological damage; intestinal damage; infertility; AIDS; SCID;
KW severe combined immunodeficiency.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= signal_peptide
FT Protein 26..245
FT /label= mature_stem_cell_factor
XX
PN US6207802-B1.
XX
PD 27-MAR-2001.
XX
PF 09-NOV-1994; 94US-0336728.
XX
PR 25-NOV-1992; 92US-0982255.
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 01-OCT-1990; 90US-0589701.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI: 2001-353108/37.
DR N-PSDB; AAF89105.
XX
PT Novel isolated non-human mammalian stem cell factor polypeptide
PT stimulating growth of early haematopoietic progenitor cells, useful for
PT treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT sarcoidosis -
XX
PS Example 5; Fig 44; 209pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC mammalian stem cell factors (SCFs). These are capable of stimulating the
CC growth of early hematopoietic progenitor cells, neural stem cells and
CC primordial germ stem cells. The sequences are useful in the treatment of
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological

CC and intestinal damage, infertility, AIDS and severe combined
CC immunodeficiency (SCID). The present sequence is an SCF described in the
CC invention.
XX
SQ Sequence 245 AA;
Query Match 100.0%; Score 1262; DB 22; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.5e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQTWLTCTCYQLLFPNPLVKTGTCRRRVTVNKKVDYTKLVANLPKDYMTLTQYVG 60
| | | | |
DB 1 MKKTQTWLTCTCYQLLFPNPLVKTGTCRRRVTVNKKVDYTKLVANLPKDYMTLTQYVG 60
| | | | |
QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDKLVNIYVDIVCEVKENSS 120
| | | | |
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDKLVNIYVDIVCEVKENSS 120
| | | | |
QY 121 KDLKKSFKSPERPLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGRKNPP 180
| | | | |
DB 121 KDLKKSFKSPERPLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGRKNPP 180
| | | | |
QY 181 GDSLSHMAAMALPALFSLIIGFAGALYWKGRPSLTRAVENIQINEEDNEISMLQEKER 240
| | | | |
DB 181 GDSLSHMAAMALPALFSLIIGFAGALYWKGRPSLTRAVENIQINEEDNEISMLQEKER 240
| | | | |
QY 241 EFOEV 245
| | | | |
DB 241 EFOEV 245
| | | | |
RESULT 9
AAB95643
ID AAB95643 standard; Protein; 245 AA.
XX
AC AAB95643;
XX
DT 05-DEC-2002 (first entry)
XX
DE Human SCF protein from 5637 bladder carcinoma cell line.
XX
XX Stem cell factor; SCF; blood-forming system; blood cell disorder;
KW hematopoietic system; metastatic carcinoma; acute leukaemia;
KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KW refractory erythroblastic anaemia;iliary tuberculosis; cytostatic;
KW disseminated fungus disease; haematopoietic; tuberculous;tic;
KW antianemic; antifungal; antimalarial; dermatological; human;
KW 5637 bladder carcinoma cell line.
XX
OS Homo sapiens.
XX
PN EP1241258-A2.
XX
PD 18-SEP-2002.
XX
PF 04-OCT-1990; 2002EP-0008587.
XX
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 28-SEP-1990; 90WO-US05548.
PR 01-OCT-1990; 90US-0589701.
PR 04-OCT-1990; 90EP-0310899.
PR 04-OCT-1990; 95EP-0105391.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX
DR WPI: 2002-684093/74.
DR N-PSDB; AAB73860.
XX
PT Production of a human stem cell factor (SCF) polypeptide for treating

PT disorders involving blood cells, such as leukaemia, comprises culturing
PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT encoding the human SCF
XX
XX Example 18; Fig 44; 120pp; English.
XX
CC The present invention relates to novel stem cell factors (SCFs),
CC polynucleotide sequences encoding the SCFs, and methods of producing
CC them. SCFs are involved in the blood-forming (haematopoietic)
CC system in mammals, particularly humans. The method of the invention
CC is useful for the production of human SCF. The stem cell factors are
CC useful to treat disorders involving blood cells e.g. metastatic
CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
CC lymphoma, refractory erythroidleastic anaemia, military tuberculosis,
CC disseminated fungus disease, malaria, and vitiligo. The present
CC sequence represents human SCF protein isolated from the 5637 bladder
CC carcinoma cell line.
XX
XX Sequence 245 AA;
SQ
Query Match 100.0%; Score 1262; DB 23; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.5e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYQLLEPNLVKTEGICRNRVTNNVQVTKLVANLPKDYMTTLKYPG 60
DB 1 MKKTQWILTCIYQLLEPNLVKTEGICRNRVTNNVQVTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPCHWISSEWVQVSDSLTDLDFKFSNISSELSNYSTIIDKLVINIVDDLVECKENSS 120
DB 61 MDVLPCHWISSEWVQVSDSLTDLDFKFSNISSELSNYSTIIDKLVINIVDDLVECKENSS 120
QY 121 KDLKSKFSKPEPRFLTFPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKAKANPP 180
DB 121 KDLKSKFSKPEPRFLTFPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKAKANPP 180
QY 181 GDSSLHMAWALPALFSLIIGFAGALYWKKQPSLTRAVENIQINEEDNEISMLQEKER 240
DB 181 GDSSLHMAWALPALFSLIIGFAGALYWKKQPSLTRAVENIQINEEDNEISMLQEKER 240
QY 241 EFQEV 245
DB 241 EFQEV 245
RESULT 10
AAE22327
ID AAE22327 standard; Protein; 245 AA.
XX
XX AAE22327;
XX
XX 25-JUL-2002 (first entry)
XX
XX Human SCF protein #3.
DE
XX Human stem cell factor; SCF protein; leucopenia; thrombocytopenia;
KM anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
KM infertility; neoplasia; myelofibrosis; myelocytoblastic disorder;
KM metastatic carcinoma; acute leukaemia; multiple myeloma; sarcolidosis;
KM Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KM Letterer-Siwe disease; refractory erythroidleastic anaemia; Kala azar;
KM Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
KM disseminated fungus disease; Fulminating septicemia; plebaldism; AIDS;
KM acquired immune deficiency syndrome; malaria; military tuberculosis;
KM pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KM Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo.
OS
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..25
FT /label= Signal_peptide
FT Protein 26..245

PT /note= "Mature human SCF protein"
XX
XX US2002018763-A1.
XX
XX 14-FEB-2002.
XX
XX 12-JAN-1998; 98US-0005243.
XX
XX 24-MAY-1995; 95US-0449653.
XX
XX (ZSERB/) ZSERB K M.
XX (BOSS/) BOSSERMAN R A.
XX (SUGS/) SUGS S V.
XX (MART/) MARTIN F H.
XX
XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX WPI; 2002-350789/38.
XX
XX N-PSDB; AAD35478.
XX
XX Novel non-naturally-occurring stem cell factor polypeptide, useful for
XX treating leucopenia, thrombocytopenia, anemia and for enhancing
XX engraftment of bone marrow during transplantation in a mammal -
XX
XX Claim 9; Fig 44; 217pp; English.
XX
XX The present invention relates to novel non-naturally-occurring stem cell
XX factor (SCF) polypeptides having an amino acid sequence sufficiently
XX duplicative of that of naturally-occurring SCF to allow possession of
XX haematopoietic biological activity of naturally occurring SCF. Sequences
XX of the invention are useful for treating leucopenia, thrombocytopenia,
XX anaemia and for enhancing bone marrow recovery in treatment of radiation,
XX engraftment of bone marrow during transplantation in mammals and chemical
XX or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
XX are also useful for treating acquired immune deficiency in a human, nerve
XX damage, neoplasia, infertility, myeloproliferative disorder, intestinal
XX damage in a mammal. SCF sequences are useful for preparing biologically
XX active polymer polypeptide adduct, for enhancing transfection of early
XX haematopoietic progenitor cells with a gene, and transfer of a gene into
XX a mammal. They are useful for treating myelofibrosis, myelocytoblastic
XX osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
XX Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
XX Letterer-Siwe disease, refractory erythroidleastic anaemia, Di Guglielmo
XX syndrome, congestive splenomegaly, Kala azar, sarcolidosis, primary
XX CC splenic pancytopenia, disseminated fungus disease, malaria, military
XX tuberculosis, Fulminating septicemia, pyridoxine deficiency, vitamin
XX B12 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
XX disorders such as plebaldism, AIDS (acquired immune deficiency syndrome)
XX and vitiligo. The present sequence is human SCF protein.
XX
XX
XX Sequence 245 AA;
SQ
Query Match 100.0%; Score 1262; DB 23; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.5e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYQLLEPNLVKTEGICRNRVTNNVQVTKLVANLPKDYMTTLKYPG 60
DB 1 MKKTQWILTCIYQLLEPNLVKTEGICRNRVTNNVQVTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPCHWISSEWVQVSDSLTDLDFKFSNISSELSNYSTIIDKLVINIVDDLVECKENSS 120
DB 61 MDVLPCHWISSEWVQVSDSLTDLDFKFSNISSELSNYSTIIDKLVINIVDDLVECKENSS 120
QY 121 KDLKSKFSKPEPRFLTFPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKAKANPP 180
DB 121 KDLKSKFSKPEPRFLTFPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKAKANPP 180
QY 181 GDSSLHMAWALPALFSLIIGFAGALYWKKQPSLTRAVENIQINEEDNEISMLQEKER 240
DB 181 GDSSLHMAWALPALFSLIIGFAGALYWKKQPSLTRAVENIQINEEDNEISMLQEKER 240
QY 241 EFQEV 245

DB 241 EFOEV 245

RESULT 11

ID AAY53285 standard; Protein; 246 AA.

AC AAY53285;

DT 27-JUL-2000 (first entry)

DE Human SCF protein isolated from the 5637 bladder carcinoma cell line.

XX Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;

KM primitive progenitor cell; haematopoietic disorder; synergic;

KW allogeneic; autologous bone marrow transplant; gene therapy;

KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;

XX cancer.

OS Homo sapiens.

PN EP92579-A1.

XX 12-APR-2000.

PD 04-OCT-1990; 99EP-0122861.

XX 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90MO-US05548.

PR 01-OCT-1990; 90US-0589701.

PR 04-OCT-1990; 90EP-0310899.

XX (AMGE-) AMGEN INC.

PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;

XX WPI; 2000-259135/23.

DR N-PSDB; AAA13715.

XX Production of hematopoietic cells suitable for administration to a

PT subject using progenitor cells and expanding the cells using stem cell

PT factor -

XX Claim 23; Fig 44; 123pp; English.

PS A method has been developed of making haematopoietic cells suitable for

XX administration to a subject. The method comprises: (a) obtaining

CC haematopoietic progenitor cells from a donor; and (b) expanding the

CC cells by adding to the cells a haematopoietically effective dose of a

CC polypeptide product having at least part of the primary structural

CC confirmation and one or more of the biological properties of naturally

CC occurring stem cell factor (SCF). The method is useful for stimulating

CC primitive progenitor cells including early haematopoietic progenitor

CC cells which are capable of maturing to erythroid, megakaryocyte,

CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute

CC increases in haematopoietic cells of both myeloid and lymphoid lineages.

CC SCF is useful for treating haematopoietic disorders. The method is

CC useful for expanding early haematopoietic progenitors in syngeneic,

CC allogeneic or autologous bone marrow transplant. SCF is useful for

CC enhancing the efficiency of gene therapy based on transfecting

CC haematopoietic stem cells. SCF is also useful for combating the

CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing

CC haematopoietic recovery after acute blood loss and as a boost to the

CC immune system for fighting neoplasia (cancer). The present sequence

CC represents a specifically claimed human SCF from the present invention.

XX Sequence 246 AA;

XX Query Match 99.2%; Score 1251.5; DB 21; Length 246;

XX Best Local Similarity 99.6%; Pred. No. 1.8e-120;

Matches 245; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKKTO-TWITLTICIVQLLFPNLYVKTBEICRRRVNNVNDYTKLVANLPKQVMTLKVP 59

DB 1 MKKTO-TWITLTICIVQLLFPNLYVKTBEICRRRVNNVNDYTKLVANLPKQVMTLKVP 60

QY 60 GMDVLPSCWISSEMVOQLSDSLTDLDFKFSNISSEGLSNYSITDKLVNIYVDLVECKENS 119

DB 61 GMDVLPSCWISSEMVOQLSDSLTDLDFKFSNISSEGLSNYSITDKLVNIYVDLVECKENS 120

QY 120 SKDLKKSFKSPPEPRLPFTPEEFPIRNSIDAFAKDFVVASSETSDCVVSTLSPKCKAKNP 179

DB 121 SKDLKKSFKSPPEPRLPFTPEEFPIRNSIDAFAKDFVVASSETSDCVVSTLSPKCKAKNP 180

QY 180 PDDSSLHMAAMALPALFSLITGFARFALYMKRQPSLRVAENIQINEDNEISMLQEK 239

DB 181 PDDSSLHMAAMALPALFSLITGFARFALYMKRQPSLRVAENIQINEDNEISMLQEK 240

QY 240 REFOEV 245

DB 241 REFOEV 246

RESULT 12

AA11711 standard; Protein; 273 AA.

AC AA11711;

DT 20-JUN-1991 (first entry)

DE Human Stem Cell Factor from HT1080 fibrosarcoma line.

KM Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FT Peptide

FT Protein

XX Location/Qualifiers

XX 1..25

XX /label= sig_peptide

XX 26..273

XX /label= mat-protein

PN EP423980-A.

XX 24-APR-1991.

PD 04-OCT-1990; 90EP-0310899.

XX 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90MO-US05548.

XX (AMGE-) AMGEN INC.

PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;

XX WPI; 1991-119233/17.

DR N-PSDB; AAQ11542.

XX New naturally-occurring polypeptide stem cell factor analogues -

PT have haematopoietic biological activity of stem cell factor and

PT are used to treat eg leukopenia, AIDS, nerve damage and

PT infertility

XX Disclosure: Fig 42; 127pp; English.

XX The SCF has the ability to stimulate growth of primitive

CC progenitors including early haematopoietic progenitor cells and non-

CC haematopoietic stem cells such as neutral stem cells and primordial

CC germ stem cells. The product may be used in a pharmaceutical

CC compen. for treating, in a mammal, leukopenia, thrombocytopenia,
 CC anaemia, AIDS, neoplasia, nerve damage, infertility and
 CC intestinal damage.
 CC See also AAR11708, AAQ1509-Q11543.

XX Sequence 273 AA;

Query Match 97.5%; Score 1231; DB 12; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2.7e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWIIITCIYLLFNPVLTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWIIITCIYLLFNPVLTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPBHCWISENVVQLSDSLTDLDKFSNISGLSYIIDKLVNIYVDLVCEKENS 120
 DB 61 MDVLPBHCWISENVVQLSDSLTDLDKFSNISGLSYIIDKLVNIYVDLVCEKENS 120
 QY 121 KDLKKSFKSPBRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKG----- 174
 DB 121 KDLKKSFKSPBRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKDSRVST 180
 QY 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 212
 DB 181 KPFLPVAASLSLRNDSSSNRKAQNPDPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
 QY 213 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 245
 DB 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273

RESULT 13

AAR20647
 ID AAR20647 standard; Protein; 273 AA.

XX AAR20647;
 AC 25-MAR-2003 (updated)
 DT 30-APR-1992 (first entry)
 XX Human mast cell growth factor.
 DE
 XX hMGF-2.4; hematopoietin; interleukin; IL-3; c-kit oncogene;
 KM proliferation.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..25
 FT /label= signal
 FT Region 26..210
 FT /label= extracellular
 FT /note= "claimed polypeptide"
 FT Region 211..237
 FT /label= transmembrane
 FT Region 238..273
 FT /label= intracellular
 XX
 XX W09200376-A.
 PN
 XX 09-JAN-1992.
 PD
 XX 14-JUN-1991; 91WO-US04274.
 PF
 XX 25-JUN-1990; 90US-0543264.
 PR 10-AUG-1990; 90US-0565840.
 PR 28-AUG-1990; 90US-0574152.
 PR 21-SEP-1990; 90US-0566073.
 PR 12-JUN-1991; 91US-0713715.
 XX
 XX (IMMV) IMMUNEX CORP.
 PA
 XX

PI Williams DE, Lyman S;
 XX
 DR MPI: 1992-041558/05.
 DR N-PSDB; AAQ20845.

XX New isolated DNA encoding human mast cell growth factor - useful in
 PT stimulating proliferation of haematopoietic cells with growth factor,
 PT to treat hemolytic and hypoproliferative anaemias
 XX
 PS Claim 10; Fig 4; 59pp; English.

CC This human MGF has a mature extracellular region of 185 amino acids.
 CC There is a second form of hMGF (see AAQ20844) resulting from an
 CC alternative mRNA splicing event which deletes an exon encoding an
 CC additional 28 amino acids beginning at amino acid 148 of the mature
 CC protein. MGF is the ligand for the protein receptor expression product
 CC of the c-kit proto-oncogene. MGF can be used to augment the
 CC activity of other cytokines. It can influence early lymphoid or
 CC myeloid development. See also AAQ20842-3 and AAQ22204-7.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 273 AA;

Query Match 97.5%; Score 1231; DB 13; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2.7e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWIIITCIYLLFNPVLTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWIIITCIYLLFNPVLTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPBHCWISENVVQLSDSLTDLDKFSNISGLSYIIDKLVNIYVDLVCEKENS 120
 DB 61 MDVLPBHCWISENVVQLSDSLTDLDKFSNISGLSYIIDKLVNIYVDLVCEKENS 120
 QY 121 KDLKKSFKSPBRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKG----- 174
 DB 121 KDLKKSFKSPBRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKDSRVST 180
 QY 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 212
 DB 181 KPFLPVAASLSLRNDSSSNRKAQNPDPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
 QY 213 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 245
 DB 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273

RESULT 14

AAR83978
 ID AAR83978 standard; Protein; 273 AA.

XX AAR83978;
 AC 25-MAR-2003 (updated)
 DT 15-MAY-1996 (first entry)
 XX Human stem cell factor derived from HT1080 fibrosarcoma cell line.
 DE
 XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
 KM thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
 KM transplant; neoplasia; myelosuppression; bone marrow; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..25
 FT /label= sig_peptide
 FT Protein 26..248
 FT /label= mat_SCF
 XX
 XX EP676470-A1.
 PN
 XX

Db	181	KPMLPPVAASLRNDSSSNRKA		240
Qy	213	QPSLTRAVENTIOINEEDNEISML		245
Db	241	QPSLTRAVENTIOINEEDNEISML		273

Search completed: February 5, 2004, 15:05:14
Job time : 35.0964 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2004, 15:03:24 ; Search time 12.8237 Seconds

(without alignments)
808.360 Million cell updates/sec

Title: US-09-224-683-63

Perfect score: 1262
Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNISMLQKEREFEV 245

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1262	100.0	245	US-08-482-918-63	Sequence 63, Appl
2	1262	100.0	245	US-09-224-681-63	Sequence 63, Appl
3	1262	100.0	245	US-08-336-728A-63	Sequence 63, Appl
4	1231	97.5	273	US-08-220-379B-2	Sequence 9, Appl
5	1231	97.5	273	US-08-628-428-9	Sequence 9, Appl
6	1231	97.5	273	US-08-482-918-49	Sequence 49, Appl
7	1231	97.5	273	US-08-482-918-61	Sequence 49, Appl
8	1231	97.5	273	US-09-224-681-49	Sequence 49, Appl
9	1231	97.5	273	US-09-224-681-61	Sequence 49, Appl
10	1231	97.5	273	US-08-336-728A-48	Sequence 48, Appl
11	1231	97.5	273	US-08-336-728A-49	Sequence 48, Appl
12	1231	97.5	273	US-08-336-728A-61	Sequence 48, Appl
13	1226	97.1	273	US-08-482-918-48	Sequence 48, Appl
14	1226	97.1	273	US-09-224-681-48	Sequence 48, Appl
15	1215	96.3	273	US-08-482-918-50	Sequence 50, Appl
16	1215	96.3	273	US-09-224-681-50	Sequence 50, Appl
17	1212	96.0	273	US-08-336-728A-50	Sequence 50, Appl
18	1099	87.1	248	US-08-955-848A-82	Sequence 82, Appl
19	1070.5	84.8	266	US-08-482-918-57	Sequence 57, Appl
20	1070.5	84.8	266	US-09-224-681-57	Sequence 57, Appl
21	1036.5	82.1	274	US-08-336-728A-57	Sequence 57, Appl
22	1036.5	82.1	274	US-08-336-728A-52	Sequence 52, Appl
23	1020.5	80.9	271	US-08-482-918-52	Sequence 52, Appl
24	1020.5	80.9	271	US-09-224-681-52	Sequence 52, Appl
25	1014.5	80.4	274	US-08-482-918-51	Sequence 51, Appl
26	1014.5	80.4	274	US-09-224-681-51	Sequence 51, Appl
27	1014.5	80.4	274	US-08-336-728A-51	Sequence 51, Appl

28	1012.5	80.2	274	US-08-336-728A-53	Sequence 53, Appl
29	1007	79.8	273	US-08-482-918-53	Sequence 53, Appl
30	1007	79.8	273	US-09-224-681-53	Sequence 53, Appl
31	992	78.6	273	US-08-482-918-42	Sequence 42, Appl
32	992	78.6	273	US-09-224-681-42	Sequence 42, Appl
33	992	78.6	273	US-08-336-728A-42	Sequence 42, Appl
34	992	78.6	273	US-08-336-728A-54	Sequence 54, Appl
35	991	78.5	273	US-08-336-728A-54	Sequence 54, Appl
36	991	78.5	273	US-08-482-918-55	Sequence 55, Appl
37	991	78.5	273	US-09-224-681-55	Sequence 55, Appl
38	991	78.5	273	US-08-336-728A-55	Sequence 55, Appl
39	985	78.1	273	US-08-482-918-54	Sequence 54, Appl
40	985	78.1	273	US-09-224-681-54	Sequence 54, Appl
41	978	77.5	273	US-08-341-456A-11	Sequence 11, Appl
42	978	77.5	273	US-08-478-414A-11	Sequence 11, Appl
43	978	77.5	273	US-08-325-240A-11	Sequence 11, Appl
44	978	77.5	273	US-08-898-982-11	Sequence 11, Appl
45	978	77.5	273	US-09-371-261-11	Sequence 11, Appl

ALIGNMENTS

```
RESULT 1
US-08-482-918-63
; Sequence 63, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zaebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-482-918-63

Query Match      100.0%; Score 1262; DB 3; Length 245;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKKTQWILTCIYLQLLFNPLVKTEGICRNEVTNNVQKVTGLVANLPKDYMITTKYVG 60
DB      1 MKKTQWILTCIYLQLLFNPLVKTEGICRNEVTNNVQKVTGLVANLPKDYMITTKYVG 60
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QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
QY 121 KDLKKSFKSPBRLPTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNPP 180
DB 121 KDLKKSFKSPBRLPTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNPP 180
QY 181 GDSLSHMAAMALPALFSLIIGFAGALYMKKROPSTRAVENIQINEEDNEISMLOEKER 240
DB 181 GDSLSHMAAMALPALFSLIIGFAGALYMKKROPSTRAVENIQINEEDNEISMLOEKER 240
QY 241 EFOEV 245
DB 241 EFOEV 245

RESULT 2
US-09-224-681-63
Sequence 63, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-63

Query Match 100.0%; Score 1262; DB 3; Length 245;
Best Local Similarity 100.0%; Pred. No. 2,6e-125;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCYLLQLLFNPVLYTEGICRRRTVNNVDYTKLVANLPRDYMILTKYVG 60
DB 1 MKKTQWILTCYLLQLLFNPVLYTEGICRRRTVNNVDYTKLVANLPRDYMILTKYVG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
QY 121 KDLKKSFKSPBRLPTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNPP 180
DB 121 KDLKKSFKSPBRLPTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNPP 180
QY 181 GDSLSHMAAMALPALFSLIIGFAGALYMKKROPSTRAVENIQINEEDNEISMLOEKER 240
DB 181 GDSLSHMAAMALPALFSLIIGFAGALYMKKROPSTRAVENIQINEEDNEISMLOEKER 240
QY 241 EFOEV 245
DB 241 EFOEV 245

RESULT 3
US-08-336-728A-63
Sequence 63, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Crough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-63

Query Match 100.0%; Score 1262; DB 3; Length 245;
Best Local Similarity 100.0%; Pred. No. 2, 6e-125;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKQTQWILTCIYQLLEFNPVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKVPG 60
DB 1 MKQTQWILTCIYQLLEFNPVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKVPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIVDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIVDDLVCEKENS 120
QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNP 180
DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNP 180
QY 181 GDSGLHWAAMALPALFSLIGFAFALYMKRQPSLTRAVENTIINEEDNEISMLQEKER 240
DB 181 GDSGLHWAAMALPALFSLIGFAFALYMKRQPSLTRAVENTIINEEDNEISMLQEKER 240
QY 241 EPOEV 245
DB 241 EPOEV 245

RESULT 4

US-08-220-379B-2
Sequence 2, Application US/08220379B
Patent No. 5525708
GENERAL INFORMATION:
APPLICANT: No. 5525708Ka, Karl
APPLICANT: Lohell, Robert B
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,379B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytomed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: cleavage site
LOCATION: 164..165
US-08-220-379B-2

Query Match 97.5%; Score 1231; DB 1; Length 273;
Best Local Similarity 89.4%; Pred. No. 5, 9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKQTQWILTCIYQLLEFNPVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKVPG 60
DB 1 MKQTQWILTCIYQLLEFNPVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKVPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIVDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVNIVDDLVCEKENS 120
QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNP 174
DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNP 180
QY 175 -----KAKPQDSSLHWAAMALPALFSLIGFAFALYMKR 212
DB 181 KPFLPVAASSLRNDSSSNRAKNPQDSSLHWAAMALPALFSLIGFAFALYMKR 240
QY 213 QPSLTRAVENTIINEEDNEISMLQEKERPOEV 245
DB 241 QPSLTRAVENTIINEEDNEISMLQEKERPOEV 273

RESULT 5

US-08-628-428-9
Sequence 9, Application US/08628428
Patent No. 585962
GENERAL INFORMATION:
APPLICANT: Lu, Hsiang
TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,428
FILING DATE: 05-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Knight, Matthew W
REGISTRATION NUMBER: 36,846
REFERENCE/DOCKET NUMBER: A-400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids

BEST AVAILABLE COPY

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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..273
OTHER INFORMATION: /note="NOTE: Mature full length
OTHER INFORMATION: 1-248 SCF protein begins at amino acid 26; amino acid 1-25
OTHER INFORMATION: include Met and leader sequences for membrane band form of hu
OTHER INFORMATION: recombinant SCF."
US-08-628-428-9

Query Match 97.5%; Score 1231; DB 2; Length 273;
Best Local Similarity 89.4%; Pred. No. 5.9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPVLTGEGICRNRVTNNVADYTKLVANPKDYMITLKYPVG 60
DB 1 MKKTQWILTCIYQLLLFNPVLTGEGICRNRVTNNVADYTKLVANPKDYMITLKYPVG 60
QY 61 MDVLPSCWISSEMVVQSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKVENS 120
DB 61 MDVLPSCWISSEMVVQSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKVENS 120
QY 121 KDLKSKFSPEPRFLTPEEFRIFNRSIDAFKDFVVASSETSDCVVSTLSPEKSG----- 174
DB 121 KDLKSKFSPEPRFLTPEEFRIFNRSIDAFKDFVVASSETSDCVVSTLSPEKSGSVSVT 180
QY 175 -----KAKNPQDSSLHMAAMALPALPSLIIGFAFGALYMKR 212
DB 181 KPFMLPVAASSLRNDSSSNRKAQNPQDSSLHMAAMALPALPSLIIGFAFGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273

RESULT 6

US-08-482-918-49
Sequence 49, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Boeselman, Robert A.
APPLICANT: Sugers, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-49

Query Match 97.5%; Score 1231; DB 3; Length 273;
Best Local Similarity 89.4%; Pred. No. 5.9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPVLTGEGICRNRVTNNVADYTKLVANPKDYMITLKYPVG 60
DB 1 MKKTQWILTCIYQLLLFNPVLTGEGICRNRVTNNVADYTKLVANPKDYMITLKYPVG 60
QY 61 MDVLPSCWISSEMVVQSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKVENS 120
DB 61 MDVLPSCWISSEMVVQSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKVENS 120
QY 121 KDLKSKFSPEPRFLTPEEFRIFNRSIDAFKDFVVASSETSDCVVSTLSPEKSG----- 174
DB 121 KDLKSKFSPEPRFLTPEEFRIFNRSIDAFKDFVVASSETSDCVVSTLSPEKSGSVSVT 180
QY 175 -----KAKNPQDSSLHMAAMALPALPSLIIGFAFGALYMKR 212
DB 181 KPFMLPVAASSLRNDSSSNRKAQNPQDSSLHMAAMALPALPSLIIGFAFGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273

RESULT 7

US-08-482-918-61
Sequence 61, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Boeselman, Robert A.
APPLICANT: Sugers, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid

BEST AVAILABLE COPY

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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-61

Query Match 97.5%; Score 1231; DB 3; Length 273;
Best Local Similarity 89.4%; Pred. No. 5.9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISBGLSNYSIIDLVNIYVDLVECVENSS 120
DB 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISBGLSNYSIIDLVNIYVDLVECVENSS 120
QY 121 KDLKSFKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSVSVT 174
DB 121 KDLKSFKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSVSVT 180
QY 175 -----KAKNPGDSSLHMAAMLPALFSLIIGFAGALYMKR 212
DB 181 KPMPLPPVAASSLRNDSSSNRAKNPBGDSLHMAAMLPALFSLIIGFAGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 245
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273

RESULT 8
US-09-224-681-49
Sequence 49, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616

FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-49

Query Match 97.5%; Score 1231; DB 3; Length 273;
Best Local Similarity 89.4%; Pred. No. 5.9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISBGLSNYSIIDLVNIYVDLVECVENSS 120
DB 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISBGLSNYSIIDLVNIYVDLVECVENSS 120
QY 121 KDLKSFKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSVSVT 174
DB 121 KDLKSFKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSVSVT 180
QY 175 -----KAKNPGDSSLHMAAMLPALFSLIIGFAGALYMKR 212
DB 181 KPMPLPPVAASSLRNDSSSNRAKNPBGDSLHMAAMLPALFSLIIGFAGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 245
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273

RESULT 9
US-09-224-681-61
Sequence 61, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

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1      CURRENT APPLICATION DATA:
2      APPLICATION NUMBER:  US/09/224,681
3      FILING DATE:
4      CLASSIFICATION:
5      PRIOR APPLICATION DATA:
6      APPLICATION NUMBER:  09/005,893
7      FILING DATE:  12-JAN-1998
8      CLASSIFICATION:
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER:  08/449,653
11     FILING DATE:  24-MAY-1995
12     CLASSIFICATION:
13     PRIOR APPLICATION DATA:
14     APPLICATION NUMBER:  07/982,255
15     FILING DATE:  25-NOV-1992
16     PRIOR APPLICATION DATA:
17     APPLICATION NUMBER:  07/589,701
18     FILING DATE:  01-OCT-1990
19     PRIOR APPLICATION DATA:
20     APPLICATION NUMBER:  07/573,616
21     FILING DATE:  24-AUG-1990
22     PRIOR APPLICATION DATA:
23     APPLICATION NUMBER:  07/537,198
24     FILING DATE:  11-JUN-1990
25     PRIOR APPLICATION DATA:
26     APPLICATION NUMBER:  07/422,383
27     FILING DATE:  16-OCT-1989
28     ATTORNEY/AGENT INFORMATION:
29     NAME:  Clough, David W.
30     REGISTRATION NUMBER:  36,107
31     REFERENCE/DOCKET NUMBER:  01017/35199
32     TELECOMMUNICATION INFORMATION:
33     TELEPHONE:  312/474-6300
34     TELEFAX:  312/474-0448
35     TELETYPE:
36     INFORMATION FOR SEQ ID NO:  61:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH:  273 amino acids
39     TYPE:  amino acid
40     TOPOLOGY:  linear
41     MOLECULE TYPE:  protein
42     US-9-224-681-61

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DB	Query Match	Best Local Similarity	Matches	244; Conservative	0; Mismatches	1; Indels	28; Gaps	1
QY	1 MKKTQWTLLTCTIYIOLLLFNPLVTEGICRRRVNNVNDVTKLVANLPRDVIITLKYPG	97.5%;	Score 1231;	DB 3;	Length 273;			60
DB	1 MKKTQWTLLTCTIYIOLLLFNPLVTEGICRRRVNNVNDVTKLVANLPRDVIITLKYPG	89.4%;	Pred. No. 5.9e-12;					60
QY	61 MDVLPSSHCHWISSENVVQSDSLTDLDDKRSNTSEGLSNYSIIDKLVINIVDDLVECKENSS							120
DB	61 MDVLPSSHCHWISSENVVQSDSLTDLDDKRSNTSEGLSNYSIIDKLVINIVDDLVECKENSS							120
QY	121 KDLKSKFSKPPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVVSTLSPEKG-----							174
DB	121 KDLKSKFSKPPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVVSTLSPEKG-----							180
QY	175 -----KAKNPQSDSLHMAANALPALPSTLIIGPAGALYMKR							212
DB	181 KPEMLPVVAASLRLNDSSSNRKANPPGSDSLHMAANALPALPSTLIIGPAGALYMKR							240

QY 213 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273

RESULT 11

US-08-336-728A-49
Sequence 49, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zaebo, Kristzina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-49

Query Match 97.5%; Score 1231; DB 3; Length 273;
Best Local Similarity 89.4%; Pred. No. 5.9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWMLTCTYQLLENPVKTBCICNRRTYNNKDYKYVANI.PKRYMTTLKVP 60
DB 1 MKKTQWMLTCTYQLLENPVKTBCICNRRTYNNKDYKYVANI.PKRYMTTLKVP 60
QY 61 MDVLPCHWCISEMWQLSDSLTDLDFKSNISEGLSNYS.IIDKLVINIVDVLVECVKENS 120

DB 61 MDVLPCHWCISEMWQLSDSLTDLDFKSNISEGLSNYS.IIDKLVINIVDVLVECVKENS 120
QY 121 KDLKSFSPERLTPPEEFRIENRSIDAFDPVVASETSCVVSSTLSPKGRS 174
DB 121 KDLKSFSPERLTPPEEFRIENRSIDAFDPVVASETSCVVSSTLSPKGRS 180
QY 175 -----KAKNPQDSSLHMAAMALPALFSLIIGFAGALYWK 212
DB 181 KPMLPVAASSLRNDSSSNKAKNPQDSSLHMAAMALPALFSLIIGFAGALYWK 240

RESULT 12

US-08-336-728A-61
Sequence 61, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zaebo, Kristzina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-61

Query Match 97.5%; Score 1231; DB 3; Length 273;
Best Local Similarity 89.4%; Pred. No. 5,9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPVKTGICRNRTNNVQVTKLVANLPKDYMITLKYPVG 60
DB 1 MKKTQWILTCIYLQLLFNPVKTGICRNRTNNVQVTKLVANLPKDYMITLKYPVG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
QY 121 KOLKSFSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKG----- 174
DB 121 KOLKSFSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKDSRVST 180
QY 175 -----KAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 212
DB 181 KPFMLPVAASLRNDSSSNRKAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273

RESULT 13

US-08-482-918-48
Sequence 48, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-48

Query Match 97.1%; Score 1226; DB 3; Length 273;
Best Local Similarity 89.0%; Pred. No. 2e-121;
Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPVKTGICRNRTNNVQVTKLVANLPKDYMITLKYPVG 60
DB 1 MKKTQWILTCIYLQLLFNPVKTGICRNRTNNVQVTKLVANLPKDYMITLKYPVG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
QY 121 KOLKSFSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKG----- 174
DB 121 KOLKSFSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKDSRVST 180
QY 175 -----KAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 212
DB 181 KPFMLPVAASLRNDSSSNRKAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273

RESULT 14

US-09-224-681-48
Sequence 48, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48

Query Match 97.1%; Score 1226; DB 3; Length 273;
Best Local Similarity 89.0%; Pred. No. 2e-121;
Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDVLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDVLVECVKENS 120
QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPEKSG----- 174
DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPEKSGSVT 180
QY 175 -----KAKNPBGSSLHMAAMLPALFSLITGFAGALYWKRR 212
DB 181 KPEMLPPVAASSLRNDSSSNRKAKNPBGSSLHMAAMLPALFSLITGFAGALYWKRR 240
QY 213 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 245
DB 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273

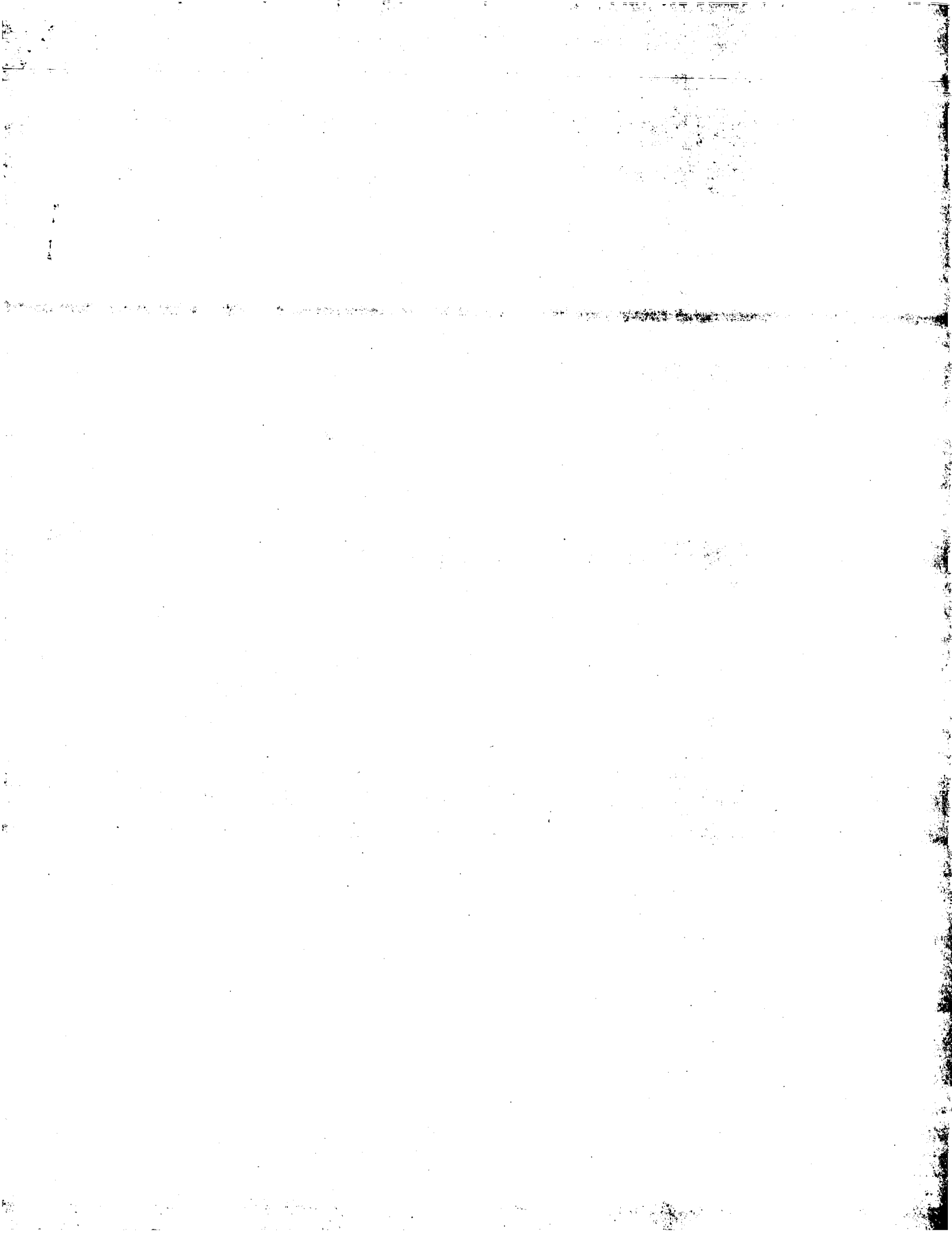
RESULT 15
US-08-482-918-50
Sequence 50, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-50

Query Match 96.3%; Score 1215; DB 3; Length 273;
Best Local Similarity 88.3%; Pred. No. 2.9e-120;
Matches 241; Conservative 0; Mismatches 4; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDVLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDVLVECVKENS 120
QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPEKSG----- 174
DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPEKSGSVT 180
QY 175 -----KAKNPBGSSLHMAAMLPALFSLITGFAGALYWKRR 212
DB 181 KPEMLPPVAASSLRNDSSSNRKAKNPBGSSLHMAAMLPALFSLITGFAGALYWKRR 240
QY 213 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 245
DB 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273

Search completed: February 5, 2004, 15:12:24
Job time: 13.8237 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:07:35 ; Search time 27.3347 Seconds
(without alignments)
1876.686 Million cell updates/sec

Title: US-09-224-683-63

Perfect score: 1262
Sequence: 1 MKKTQTWILTCIYLQLLFN.....NEEDNEISMLQEKEREFQEV 245

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Published Applications_AA:*
- 2: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
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- 8: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1262	100.0	245	US-09-005-243-63	Sequence 63, Appl
2	1262	100.0	245	US-09-224-683-63	Sequence 63, Appl
3	1231	97.5	273	US-09-005-243-49	Sequence 49, Appl
4	1231	97.5	273	US-09-005-243-61	Sequence 61, Appl
5	1231	97.5	273	US-09-224-683-49	Sequence 49, Appl
6	1231	97.5	273	US-09-224-683-61	Sequence 61, Appl
7	1226	97.1	273	US-09-005-243-48	Sequence 48, Appl
8	1226	97.1	273	US-09-224-683-48	Sequence 48, Appl
9	1215	96.3	273	US-09-005-243-50	Sequence 50, Appl
10	1215	96.3	273	US-09-224-683-50	Sequence 50, Appl
11	1070.5	84.8	266	US-09-005-243-57	Sequence 57, Appl
12	1070.5	84.8	266	US-09-224-683-57	Sequence 57, Appl
13	1020.5	80.9	271	US-09-005-243-52	Sequence 52, Appl
14	1020.5	80.9	271	US-09-224-683-52	Sequence 52, Appl
15	1014.5	80.4	274	US-09-005-243-51	Sequence 51, Appl

16	1014.5	80.4	274	US-09-224-683-51	Sequence 51, Appl
17	1007	79.8	273	US-09-005-243-53	Sequence 53, Appl
18	1007	79.8	273	US-09-224-683-53	Sequence 53, Appl
19	992	78.6	273	US-09-005-243-42	Sequence 42, Appl
20	992	78.6	273	US-09-224-683-42	Sequence 42, Appl
21	991	78.5	273	US-09-005-243-55	Sequence 55, Appl
22	991	78.5	273	US-09-224-683-55	Sequence 55, Appl
23	991	78.5	273	US-10-132-345-4	Sequence 4, Appl
24	985	78.1	273	US-09-005-243-54	Sequence 54, Appl
25	985	78.1	273	US-09-224-683-54	Sequence 54, Appl
26	900	71.3	270	US-10-132-345-2	Sequence 2, Appl
27	890	70.5	208	US-09-005-243-46	Sequence 46, Appl
28	890	70.5	208	US-09-224-683-46	Sequence 46, Appl
29	865	68.5	195	US-09-005-243-44	Sequence 44, Appl
30	865	68.5	195	US-09-224-683-44	Sequence 44, Appl
31	758	60.1	164	US-09-903-327A-10	Sequence 10, Appl
32	758	60.1	165	US-10-320-231A-25	Sequence 25, Appl
33	758	60.1	165	US-10-053-355A-2	Sequence 2, Appl
34	758	60.1	165	US-10-053-355A-2	Sequence 2, Appl
35	758	60.1	166	US-09-748-592-2	Sequence 2, Appl
36	756	59.9	193	US-10-270-555-1	Sequence 1, Appl
37	696	55.2	196	US-09-903-327A-14	Sequence 14, Appl
38	636	55.2	196	US-09-005-243-40	Sequence 40, Appl
39	594	47.1	165	US-09-224-683-40	Sequence 40, Appl
40	594	47.1	165	US-09-005-243-41	Sequence 1, Appl
41	586	46.4	393	US-10-270-555-2	Sequence 2, Appl
42	564	44.7	282	US-09-005-243-56	Sequence 56, Appl
43	564	44.7	282	US-09-224-683-56	Sequence 56, Appl
44	281	22.3	56	US-10-176-791A-61	Sequence 61, Appl
45	266	21.1	56	US-10-176-791A-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
US-09-005-243-63
; Sequence 63, Application US/09005243
; Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristzina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor.
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/569,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-63

Query Match 100.0%; Score 1262; DB 9; Length 245;
Best Local Similarity 100.0%; Pred. No. 5,1e-119;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLDPKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDPKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDLKSFSPKPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKGAKNPP 180
DB 121 KDLKSFSPKPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKGAKNPP 180
QY 181 GDSLSHMAAMALPALFSLIIGFAGALYWKRSQPSLTRAVERNIOINEEDNEISMLQEKER 240
DB 181 GDSLSHMAAMALPALFSLIIGFAGALYWKRSQPSLTRAVERNIOINEEDNEISMLQEKER 240
QY 241 EFOEV 245
DB 241 EFOEV 245

RESULT 2

US-09-224-683-63
Sequence 63, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Boeselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-63

Query Match 100.0%; Score 1262; DB 9; Length 245;
Best Local Similarity 100.0%; Pred. No. 5,1e-119;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLDPKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDPKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDLKSFSPKPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKGAKNPP 180
DB 121 KDLKSFSPKPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKGAKNPP 180
QY 181 GDSLSHMAAMALPALFSLIIGFAGALYWKRSQPSLTRAVERNIOINEEDNEISMLQEKER 240
DB 181 GDSLSHMAAMALPALFSLIIGFAGALYWKRSQPSLTRAVERNIOINEEDNEISMLQEKER 240
QY 241 EFOEV 245
DB 241 EFOEV 245

RESULT 3

US-09-005-243-49
Sequence 49, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.

APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-49

Query Match 97.5%; Score 1231; DB 9; Length 273;
Best Local Similarity 89.4%; Pred. No. 8.1e-116;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWIIITLCITLQILLNPVLYKTGICGNRVNNAVQVTKLVANLPKDYMTLLKVVVG 60
DB 1 MKKTQWIIITLCITLQILLNPVLYKTGICGNRVNNAVQVTKLVANLPKDYMTLLKVVVG 60
QY 61 MDVLPSCWISSEWVVDLSLTDLDKFSNISSEGLSNYSIIDLVNIIVDLVECVKENSS 120
DB 61 MDVLPSCWISSEWVVDLSLTDLDKFSNISSEGLSNYSIIDLVNIIVDLVECVKENSS 120
QY 121 KDLKSKFSKSPPLFTPEEFRRIFNNSIDAFKDPVVAASSTSDCVVSGTTSPEKGV----- 174
DB 121 KDLKSKFSKSPPLFTPEEFRRIFNNSIDAFKDPVVAASSTSDCVVSGTTSPEKGRVSVY 180

QY 175 -----KANNPGDSSLHMAANALPALPSLLIGFAGALYWKRR 212
DB 181 KPFMLPVAASSLRNDSSSNRKANNPPGDSLSLHMAANALPALPSLLIGFAGALYWKRR 240
QY 213 QPSLTRAVENTQINEDNEISMLOKEREPOEV 245
DB 241 QPSLTRAVENTQINEDNEISMLOKEREPOEV 273

RESULT 4
US-09-005-243-61
Sequence 61, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-61

Query Match 97.5%; Score 1231; DB 9; Length 273;
Best Local Similarity 89.4%; Pred. No. 8.1e-116;

Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQDVKLVANLPKDYMITLKYVPG 60
1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQDVKLVANLPKDYMITLKYVPG 60
Db 1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQDVKLVANLPKDYMITLKYVPG 60

QY 61 MDVLPSCWISBMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
61 MDVLPSCWISBMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
Db 61 MDVLPSCWISBMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120

QY 121 KDLKSFSPKSPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 174
121 KDLKSFSPKSPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 174
Db 121 KDLKSFSPKSPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180

QY 175 -----KAKNPPGSSSLHMAAMALPALPSLIIGFAGALYWKRR 212
175 -----KAKNPPGSSSLHMAAMALPALPSLIIGFAGALYWKRR 212
Db 181 KPFMLPVAASLRNDSSSNRKAKNPGDSSLHMAAMALPALPSLIIGFAGALYWKRR 240

QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 5
US-09-224-683-49
Sequence 49, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/557,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-0448
TELEFAX: 312/474-6300
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-49

Query Match 97.5%; Score 1231; DB 9; Length 273;
Best Local Similarity 89.4%; Pred. No. 8.1e-116;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQDVKLVANLPKDYMITLKYVPG 60
1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQDVKLVANLPKDYMITLKYVPG 60
Db 1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQDVKLVANLPKDYMITLKYVPG 60

QY 61 MDVLPSCWISBMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
61 MDVLPSCWISBMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
Db 61 MDVLPSCWISBMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120

QY 121 KDLKSFSPKSPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 174
121 KDLKSFSPKSPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 174
Db 121 KDLKSFSPKSPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180

QY 175 -----KAKNPPGSSSLHMAAMALPALPSLIIGFAGALYWKRR 212
175 -----KAKNPPGSSSLHMAAMALPALPSLIIGFAGALYWKRR 212
Db 181 KPFMLPVAASLRNDSSSNRKAKNPGDSSLHMAAMALPALPSLIIGFAGALYWKRR 240

QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 6
US-09-224-683-61
Sequence 61, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/449,653
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/982,255
 FILING DATE: 25-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/589,701
 FILING DATE: 01-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/573,616
 FILING DATE: 24-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/537,198
 FILING DATE: 11-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/422,383
 FILING DATE: 16-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 01017/35136
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-224-683-61

Query Match 97.5%; Score 1231; DB 9; Length 273;
 Best Local Similarity 89.4%; Pred. No. 8.1e-116;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRTNNKQVTKLVANLPKQYMTLTKYVG 60
 DB 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRTNNKQVTKLVANLPKQYMTLTKYVG 60
 QY 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
 DB 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
 QY 121 KDKKSFSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKGR----- 174
 DB 121 KDKKSFSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKGRSVYT 180
 QY 175 -----KAKNPDGSSLIHMAAMLPALFSLIIGFAGALYWK 212
 DB 181 KPFLPVAASLRNDSSSNRKAKNPDGSSLIHMAAMLPALFSLIIGFAGALYWK 240
 QY 213 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 245
 DB 241 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 273

RESULT 7
 US-09-005-243-48
 Sequence 48: Application US/09005243
 Patent No. US20020018763A1
 GENERAL INFORMATION:
 APPLICANT: Zeebo, Kristina M.
 APPLICANT: Bosseman, Robert A.
 APPLICANT: Suggs, Sidney V.
 APPLICANT: Martin, Francis H.
 TITLE OF INVENTION: Stem Cell Factor
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/005,243
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/449,653
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/982,255
 FILING DATE: 25-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/589,701
 FILING DATE: 01-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/573,616
 FILING DATE: 24-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/537,198
 FILING DATE: 11-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/422,383
 FILING DATE: 16-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 01017/34465
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-005-243-48

Query Match 97.1%; Score 1226; DB 9; Length 273;
 Best Local Similarity 89.0%; Pred. No. 2.6e-115;
 Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRTNNKQVTKLVANLPKQYMTLTKYVG 60
 DB 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRTNNKQVTKLVANLPKQYMTLTKYVG 60
 QY 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
 DB 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
 QY 121 KDKKSFSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKGR----- 174
 DB 121 KDKKSFSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKGRSVYT 180
 QY 175 -----KAKNPDGSSLIHMAAMLPALFSLIIGFAGALYWK 212
 DB 181 KPFLPVAASLRNDSSSNRKAKNPDGSSLIHMAAMLPALFSLIIGFAGALYWK 240
 QY 213 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 245
 DB 241 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 273

RESULT 8
US-09-224-683-48
Sequence 48, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-48

Query Match 97.1%; Score 1226; DB 9; Length 273;
Best Local Similarity 89.0%; Pred. No. 2.6e-115;
Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;
1 MKKTQWILTCIYQLLEFNPVKTGICRNRTNNVQVTKLVANLPKDYMITLKYYVG 60
|||||

Db 1 MKKTQWILTCIYQLLEFNPVKTGICRNRTNNVQVTKLVANLPKDYMITLKYYVG 60
QY 61 MOVLPSCHESEMVQVQSDSLTDLDKFSNTSEGLSNYSIIDKLVNIYDDIVECKENSS 120
Db 61 MOVLPSCHESEMVQVQSDSLTDLDKFSNTSEGLSNYSIIDKLVNIYDDIVECKENSS 120
QY 121 KDLKSFSPPEPRLTPEEPFRIPNRSIDAFKDFVAVSETSDCVVSTLSPEKG----- 174
Db 121 KDLKSFSPPEPRLTPEEPFRIPNRSIDAFKDFVAVSETSDCVVSTLSPEKDSRVST 180
QY 175 -----KANPPQDSGLHMANALPALFSLIIGFAGALYMKR 212
Db 181 KEFMLPVAASGLRNDSSSNRKANPPGDSLSLHWPAMALPALFSLIIGFAGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLQEKEREPOEV 245
Db 241 QPSLTRAVENTIQINEEDNEISMLQEKEREPOEV 273

RESULT 9
US-09-005-243-50
Sequence 50, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-50

Query Match 96.3%; Score 1215; DB 9; Length 273;
Best Local Similarity 88.3%; Pred. No. 3.3e-114;
Matches 241; Conservative 0; Mismatches 4; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPVLTKEGICRNRYTNVNDVTKLVANLPDQWITLTKYVG 60
DB 1 MKKTQWILTCIYQLLLFNPVLTKEGICRNRYTNVNDVTKLVANLPDQWITLTKYVG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
QY 121 KDLKSPKSPERLFTPEEFRIFNRSIDAFKDFVAVASSTDCVSVSTLSPKGRSVST 174
DB 121 KDLKSPKSPERLFTPEEFRIFNRSIDAFKDFVAVASSTDCVSVSTLSPKGRSVST 180
QY 175 -----KAKNPQDSSLHMAAALPALFSLIIGPAGALYMKR 212
DB 181 KPEMLPVAASSLRNDSSSNRKAKNPTGDSLSHMAAALPALFSLIIGPAGALYMKR 240
QY 213 QPSLTRAVENTIOINEDNEISMLQEKEREFQEV 245
DB 241 QPSLTRAVENTIOINEDNEISMLQEKEREFQEV 273

RESULT 10
US-09-224-683-50
Sequence 50, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6500
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-50

Query Match 96.3%; Score 1215; DB 9; Length 273;
Best Local Similarity 88.3%; Pred. No. 3.3e-114;
Matches 241; Conservative 0; Mismatches 4; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPVLTKEGICRNRYTNVNDVTKLVANLPDQWITLTKYVG 60
DB 1 MKKTQWILTCIYQLLLFNPVLTKEGICRNRYTNVNDVTKLVANLPDQWITLTKYVG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
QY 121 KDLKSPKSPERLFTPEEFRIFNRSIDAFKDFVAVASSTDCVSVSTLSPKGRSVST 174
DB 121 KDLKSPKSPERLFTPEEFRIFNRSIDAFKDFVAVASSTDCVSVSTLSPKGRSVST 180
QY 175 -----KAKNPQDSSLHMAAALPALFSLIIGPAGALYMKR 212
DB 181 KPEMLPVAASSLRNDSSSNRKAKNPTGDSLSHMAAALPALFSLIIGPAGALYMKR 240
QY 213 QPSLTRAVENTIOINEDNEISMLQEKEREFQEV 245
DB 241 QPSLTRAVENTIOINEDNEISMLQEKEREFQEV 273

RESULT 11
US-09-005-243-57
Sequence 57, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-57

Query Match      84.8%; Score 1070.5; DB 9; Length 266;
Best Local Similarity 82.2%; Pred. No. 1.2e-99;
Matches 222; Conservative 10; Mismatches 9; Indels 29; Gaps 6;
```

```
APPLICANT: Zeebo, Krzyszina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-57

Query Match      84.8%; Score 1070.5; DB 9; Length 266;
Best Local Similarity 82.2%; Pred. No. 1.2e-99;
Matches 222; Conservative 10; Mismatches 9; Indels 29; Gaps 6;
```


PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-52

Query Match 80.4%; Score 1020.5; DB 9; Length 271;
Best Local Similarity 75.6%; Pred. No. 1.4e-94;
Matches 205; Conservative 18; Mismatches 19; Indels 29; Gaps 3;

QY 3 KTQTWLTCTCYLQLLFNPVKTGICRNRVTNNVADVTKLVANLPKDYMTLKYPGMD 62
DB 2 KTQTWLTCTCYLQ-LLFNPVKTGICRNRVTDDVDVTKLVANLPKDYMTLKYPGMD 60
QY 63 VLPSHCWISWVQVQSLDLDLDFKPSNISEGLSNYSIIDKLVNIYDDIVECKENSSKD 122
DB 61 VLPSHCWISWVQVQSLDLDLDFKPSNISEGLSNYSIIDKLVNIYDDIVECKENSSKD 120
QY 123 LKKSFKSPERLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPEK----- 173
DB 121 VKKSKSPERLFTPEEPFRIFNRSIDAFKDFLKVMSKSECVSSTLSPEKSRVSVTK 180
QY 174 -----GKAKNPGRDSSLMHMAALPALFSLIIGFAFGALYMKKRP 214
DB 181 PFMPLPVAASSLRNDSSSNRKNTPEDSSIQMAVVALPACFSLVIGFAFGALYMKKRP 240
QY 215 SLTRAVENTIQINEEDNEISMLOEKEREFQEV 245
DB 241 NLRTVENVIQINEEDNEISMLOEKEREFQEV 271

RESULT 15
US-09-005-243-51
Sequence 51, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-51

Query Match 80.4%; Score 1014.5; DB 9; Length 274;
Best Local Similarity 74.8%; Pred. No. 5.8e-94;
Matches 205; Conservative 17; Mismatches 23; Indels 29; Gaps 2;

QY 1 MKQTWLTCTCYLQLLFNPVKTGICRNRVTNNVADVTKLVANLPKDYMTLKYPG 60
DB 1 MKQTWLTCTCYLQLLFNPVKTGICRNRVTDDVDVTKLVANLPKDYMTLKYPG 60
QY 61 MDVLPSCWISWVQVQSLDLDLDFKPSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
DB 61 MDVLPSCWISWVQVQSLDLDLDFKPSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
QY 121 KDKSKSPERLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPEK----- 174
DB 121 ENVKAPKSPERLFTPEEPFRIFNRSIDAFKDFLKVMSKSECVSSTLSPEKSRVSV 180
QY 175 -----KAKNPGRDSSLMHMAALPALFSLIIGFAFGALYMKK 211
DB 181 TKPMLPVAASSLRNDSSSNRKNTPEDSSIQMAVVALPACFSLVIGFAFGALYMKK 240
QY 212 RQPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 245
DB 241 RQPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 274

Search completed: February 5, 2004, 15:23:27
Job time: 27.3347 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 5, 2004, 15:00:43 / Search time 13.8361 Seconds
(without alignments)
1702.889 Million cell updates/sec

Title: US-09-224-683-63

Perfect score: 1262
Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISMLQEKREPOEV 245

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1262	100.0	245	2 B61190	mast cell growth f
2	1231	97.5	273	2 A35974	mast cell growth f
3	1037.5	82.2	274	2 I46575	c-kit ligand - pig
4	1022	81.0	245	2 A37934	mast cell growth f
5	1018.5	80.7	274	2 S47571	stem cell factor,
6	1014.5	80.4	274	2 I46929	stem cell factor -
7	991	78.5	273	2 S65801	stem cell factor f
8	749.5	59.4	202	2 S58513	stem cell factor p
9	721	57.1	201	2 B35974	stem cell factor p
10	605	47.9	253	2 S70367	stem cell factor s
11	584	46.3	287	2 JN0637	stem cell factor p
12	583	46.2	287	2 S70366	stem cell factor p
13	491.5	38.9	124	2 S29052	stem cell factor l
14	175.5	13.9	49	2 B35971	stem cell factor -
15	172.5	13.7	51	2 A35971	mast cell growth f
16	97.5	7.7	402	2 T09062	probable advanced
17	97	7.7	482	2 S37845	transcription init
18	97	7.7	1447	2 F82909	hypothetical prote
19	93.5	7.4	647	2 P90595	conserved hypotet
20	93.5	7.4	3227	2 T37964	probable ubiquitin
21	92.5	7.3	512	2 G86773	citrate (pro-3S) -
22	92.5	7.3	534	2 T23425	hypothetical prote
23	92	7.3	420	2 E90553	hypothetical prote
24	92	7.3	821	2 AD1507	probable secreted
25	92	7.3	1174	1 H3BYDH	helicase (EC 3.6.1
26	91.5	7.3	295	2 AC2939	hypothetical prote
27	91.5	7.3	309	2 D98343	lactose transport
28	91.5	7.3	1993	2 T30902	sodium channel SCA
29	91	7.2	378	2 F64300	formate dehydrogen

30	90.5	7.2	616	2 A69136	ATP-dependent Clp
31	90.5	7.2	774	2 T22309	hypothetical prote
32	90.5	7.2	1675	2 S70770	hypothetical prote
33	90	7.1	411	2 B72012	conserved hypotet
34	90	7.1	1	2 C86613	hypothetical prote
35	89	7.1	1384	2 T26656	hypothetical prote
36	89	7.1	2238	1 RRVUBY	genome polyprotein
37	88.5	7.0	941	2 H84855	phosphoenolpyruvat
38	88.5	7.0	1154	2 F71856	hypothetical prote
39	88	7.0	447	2 S74840	hypothetical prote
40	87.5	6.9	246	2 T19850	replication initia
41	87.5	6.9	570	2 S51404	hypothetical prote
42	87.5	6.9	966	2 S26235	phosphoenolpyruvat
43	87.5	6.9	1293	2 T27886	hypothetical prote
44	87.5	6.9	1813	2 T19295	hypothetical prote
45	87	6.9	660	2 T22794	hypothetical prote

ALIGNMENTS

RESULT 1.

B61190
mast cell growth factor, short form precursor - human
N:Alternate names: Kit ligand, short form; stem cell factor, short form
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C:Accession: B61190
R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpe, S.; Eisenman, J.; Cannizzaro, L
Cell Growth Differ. 2, 373-378, 1991
A>Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiza
A:Reference number: A61190; MUID:92172791; PMID:1724381
A:Accession: B61190
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-245 <AND>
A:Comment: Alternative splicing produces this short form in which a predicted cleavage s
C:Genetics:
A:Gene: GDB:MGF
A:Cross-references: GDB:128026; OMIM:184745
A:Map position: 12q22-12q22
A:Superfamily: mouse mast cell growth factor
C:Keywords: alternative splicing; glycoprotein; transmembrane protein
F:187-209/Domain: signal sequence #status predicted <SIG>
F:90,97,118,145/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match

Best Local Similarity 100.0%; Score 1262; DB 2; Length 245;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVDYTKLVANLPDYMITLKYPVG	60
DB	1	MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVDYTKLVANLPDYMITLKYPVG	60
QY	61	MDVLPSCWISPMVQLSDSLTDLDDKSNISSEGSNTSIIDKLVNIYDDLVCEYKENS	120
DB	61	MDVLPSCWISPMVQLSDSLTDLDDKSNISSEGSNTSIIDKLVNIYDDLVCEYKENS	120
QY	121	KOLKSFSPSPRLTPEEPFRIIPNRSIDAFQDFVAVSETSCVASTLSPKGRAXNP	180
DB	121	KOLKSFSPSPRLTPEEPFRIIPNRSIDAFQDFVAVSETSCVASTLSPKGRAXNP	180
QY	181	GDSLSHMAAMALPALFSIIGFAGALYWKROPSLTRAVENTIQINEEDNEISMLQEKER	240
DB	181	GDSLSHMAAMALPALFSIIGFAGALYWKROPSLTRAVENTIQINEEDNEISMLQEKER	240
QY	241	EFQEV 245	
DB	241	EFQEV 245	

RESULT 2

A35974
 mast cell growth factor precursor - human
 N.Alternate names: kit ligand; stem cell factor
 C.Species: Homo sapiens (man)
 C.Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
 C.Accession: A35974; A61190
 R.Martin, F.H.; Sugars, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
 s, J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, R.
 Cell 63, 203-211, 1990
 A.Title: Primary structure and functional expression of rat and human stem cell factor
 A.Reference number: A35974; MUID:91004219; PMID:2208279
 A.Molecule type: mRNA
 A.Residues: 1-273 <MAR>
 A.Cross-references: GB:M59664; NID:9337933; PIDN:AAA85450.1; PID:9337934
 R.Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimbel, S.; Eisenman, J.; Cammizzaro, I.
 Cell Growth Differ. 2, 373-378, 1991
 A.Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiza
 A.Reference number: A61190; MUID:92172791; PMID:1724381
 A.Accession: A61190
 A.Status: nucleic acid sequence not shown; not compared with conceptual translation
 A.Molecule type: mRNA
 A.Residues: 1-273 <AND>
 C.Gene: GDB:MGF
 A.Cross-references: GDB:128026; OMIM:184745
 A.Map position: 12q22-12q22
 C.Superfamily: mouse mast cell growth factor
 C.Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane pro
 F.1-25/Domain: signal sequence #status predicted <Sig>
 F.26-273/Product: mast cell growth factor #status predicted <MCS>
 F.26-189/Product: (or 26-190) mast cell growth factor; soluble form #status predicted <M
 F.215-237/Domain: transmembrane #status predicted <TM>
 F.190,97,118,145,195/Binding site: carbohydrate (Aam) (covalent) #status predicted

Query Match 97.5%; Score 1231; DB 2; Length 273;
 Best Local Similarity 89.4%; Pred. No. 1.9e-92;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLNFPLVKTGICRRRTNNVQVTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWTLTCTIYQLLNFPLVKTGICRRRTNNVQVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVINIVDDLVCEKENS 120
 DB 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVINIVDDLVCEKENS 120
 QY 121 KDLKSFSPKPEPRLLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKGV----- 174
 DB 121 KDLKSFSPKPEPRLLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKGV----- 174
 QY 175 -----KAKNPPGDSLSHMAAMLPALFSLITGPAFGALYMKR 212
 DB 181 KPEFMLPVAASLSLRNDSSSNRKAQNPDPGSSLSHMAAMLPALFSLITGPAFGALYMKR 240
 QY 213 OPSLTRAVENTIOINEEDNEISMLOEKERFQEV 245
 DB 241 OPSLTRAVENTIOINEEDNEISMLOEKERFQEV 273

RESULT 3
 146575
 C-kit ligand - pig
 C.Species: Sus scrofa domestica (domestic pig)
 C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
 C.Accession: 146575
 R.Zhang, Z.; Anthony, R.V.
 Biol. Reprod. 50, 95-102, 1994
 A.Title: Porcine stem cell factor/C-kit ligand: its molecular cloning and localization w
 A.Reference number: 146575; MUID:94146218; PMID:7508758
 A.Accession: 146575
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA

A.Residues: 1-274 <ZHA>
 A.Cross-references: GB:L07786; NID:9164420; PIDN:AAA53670.1; PID:9164421
 C.Superfamily: mouse mast cell growth factor

Query Match 82.2%; Score 1037.5; DB 2; Length 274;
 Best Local Similarity 75.2%; Pred. No. 9.6e-77;
 Matches 206; Conservative 22; Mismatches 17; Indels 29; Gaps 2;

QY 1 MKKTQWTLTCTIYQLLNFPLVKTGICRRRTNNVQVTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWTLTCTIYQLLNFPLVKTGICRRRTNNVQVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVINIVDDLVCEKENS 120
 DB 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVINIVDDLVCEKENS 120
 QY 121 KDLKSFSPKPEPRLLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKGV----- 174
 DB 121 ENVKSSKSPKPEPRLLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKGV----- 180
 QY 175 -----KAKNPPGDSLSHMAAMLPALFSLITGPAFGALYMKR 211
 DB 181 TKPFMLPVAASLSLRNDSSSNRKAQNPDPGSSLSHMAAMLPALFSLITGPAFGALYMKR 240
 QY 212 ROPSLTRAVENTIOINEEDNEISMLOEKERFQEV 245
 DB 241 KQPNLTRAVENIOINEEDNEISMLOEKERFQEV 274

RESULT 4
 A37934
 mast cell growth factor precursor (version 2) - mouse
 N.Alternate names: KL-2 protein
 C.Species: Mus musculus (house mouse)
 C.Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000
 C.Accession: A37934; B43751
 R.Flanagan, J.G.; Chan, D.C.; Leder, P.
 Cell 64, 1025-1035, 1991
 A.Title: Transmembrane form of the kit ligand growth factor is determined by alternative
 A.Reference number: A37934; MUID:91160046; PMID:1705866
 A.Accession: A37934
 A.Molecule type: mRNA
 A.Residues: 1-245 <FLA>
 A.Cross-references: GB:M64262
 R.Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992
 A.Title: Differential expression and processing of two cell associated forms of the kit-
 A.Reference number: A43751; MUID:92330001; PMID:1378327
 A.Accession: B43751
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 1-173,'R',175-186,'L',188-245 <HDA>
 A.Cross-references: GB:S04534
 A.Note: the authors translated the codon TTG for residue 187 as Trp
 C.Superfamily: mouse mast cell growth factor

Query Match 81.0%; Score 1022; DB 2; Length 245;
 Best Local Similarity 80.8%; Pred. No. 1.5e-75;
 Matches 198; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLNFPLVKTGICRRRTNNVQVTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWTLTCTIYQLLNFPLVKTGICGNPVDNDVITKLVANLPKDYMITLNTYAG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVINIVDDLVCEKENS 120
 DB 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVINIVDDLVCEKENS 120
 QY 121 KDLKSFSPKPEPRLLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKGV----- 180
 DB 121 KNKESPPKPEPRLLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKGV----- 180
 QY 181 GDSLSHMAAMLPALFSLITGPAFGALYMKRQPSLTRAVENTIOINEEDNEISMLOEKER 240

Db 181 EDGGLMTAMALPALISLVIGFAGALYMKOSILTRAVENTQINEEDNEISMLQOKR 240
 QY 241 EFOEV 245
 Db 241 EFOEV 245

RESULT 5

stem cell factor, longer isoform - bovine
 S47571
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
 C/Accession: S47571
 R/Zhou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
 Biochim. Biophys. Acta 1223, 148-150, 1994
 A/Title: Cloning and characterization of cDNAs encoding two normal isoforms of bovine st
 A/Reference number: S47571; MUID:94339176; PMID:7520283
 A/Accession: S47571
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-274 <ZHO>
 A/Cross-references: EMBL:D89934; NID:g538520; PIDN:BA06061.1; PID:g538521
 C/Superfamily: mouse mast cell growth factor

Query Match 80.7%; Score 1018.5; DB 2; Length 274;
 Best Local Similarity 74.1%; Pred. No. 3.3e-75;
 Matches 203; Conservative 20; Mismatches 22; Indels 29; Gaps 2;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICGNRVTVNNKDVTKLVANLPKQYMITLKYPG 60
 Db 1 MKKTQWILTCIYQLLFPNPLVHTQICGNRVTVDDKDVTKLVANLPKQYMITLKYPG 60
 QY 61 MDVLPSCWISSEWVQSLDSDLTDLDFKSNISSEGLSYCIIDKLVKIVDVLVECKENSS 120
 Db 61 MDVLPSCWISSEWVQSLDSDLDFKSNISSEGLSYCIIDKLVKIVDVLVECKEHS 120
 QY 121 KDLKKSFKSPERLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKSG----- 174
 Db 121 ENVKKSKSPERQFTPEKFFGIFNKSIDAFKDLVAVASGMSCEVISTSPKDSRVSV 180
 QY 175 -----KAKNPPGDSLSHMAAMALPALFSIIIGFAGALYMK 211
 Db 181 TKPFMLPVAASLSLRNDSSSNRKASNSIDSSIQMAVALPAFFSLVIGFAGAFYMK 240
 QY 212 RQPSLTRAVENTQINEEDNEISMLQOKERFQEV 245
 Db 241 KQPNLTRVTENQINEEDNEISMLQOKERFQEV 274

RESULT 6

146929
 stem cell factor - dog
 C/Species: Canis lupus familiaris (dog)
 C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jul-2000
 C/Accession: 146929
 R/Shull, R.M.; Suggs, S.V.; Langley, K.E.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
 Exp. Hematol. 20, 1118-1124, 1992
 A/Title: Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic p
 A/Reference number: 146929; MUID:93106145; PMID:1281786
 A/Accession: 146929
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-274 <SHU>
 A/Cross-references: GB:S53229; NID:g262240; PIDN:AA824619.1; PID:g262241
 C/Superfamily: mouse mast cell growth factor

Query Match 80.4%; Score 1014.5; DB 2; Length 274;
 Best Local Similarity 74.8%; Pred. No. 7e-75;
 Matches 203; Conservative 17; Mismatches 23; Indels 29; Gaps 2;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICGNRVTVNNKDVTKLVANLPKQYMITLKYPG 60
 Db 1 MKKTQWILTCIYQLLFPNPLVHTQICGNRVTVDDKDVTKLVANLPKQYMITLKYPG 60

Db 1 MKKTQWILTCIYQLLFPNPLVTKGICGNRVTVDDKDVTKLVANLPKQYKIALKYVG 60
 QY 61 MDVLPSCWISSEWVQSLDSDLDFKSNISSEGLSNYSIIDKLVNIVDVLVECKENSS 120
 Db 61 MDVLPSCWISSEWVQSLDSDLDFKSNISSEGLSNYSIIDKLVNIVDVLVECKEHS 120
 QY 121 KDLKKSFKSPERLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKSG----- 174
 Db 121 ENVKKSKSPERLFTPEEFRIFNRSIDAFKDLVAVASGMSCEVISTSPKDSRVSV 180
 QY 175 -----KAKNPPGDSLSHMAAMALPALFSIIIGFAGALYMK 211
 Db 181 TKPFMLPVAASLSLRNDSSSNRKASNSIDSSIQMAVALPAFFSLVIGFAGALYMK 240
 QY 212 RQPSLTRAVENTQINEEDNEISMLQOKERFQEV 245
 Db 241 KQPNLTRVTENQINEEDNEISMLQOKERFQEV 274

RESULT 7

stem cell growth factor - mouse
 S65801
 N/Alternate names: hematopoietic growth factor K1; ligand steel factor; stem cell facto
 C/Species: Mus musculus (house mouse)
 C/Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 01-Dec-2000
 C/Accession: S65801; A43751; A35976; A35972; A35973; A48768
 R/Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
 Genetics 142, 927-934, 1996

A/Title: Multiple pathways for Steel regulation suggested by genomic and sequence analy
 A/Reference number: S65801; MUID:97002551; PMID:884989
 A/Accession: S65801
 A/Status: preliminary
 A/Molecule type: mRNA

A/Residues: 1-273 <BED>
 A/Cross-references: EMBL:U44725; NID:g1172215; PIDN:ACG2447.1; PID:g1172216
 R/Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992

A/Title: Differential expression and processing of two cell associated forms of the kit
 A/Reference number: A43751; MUID:92330001; PMID:1378927
 A/Accession: A43751

A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-214, 'L', 216-273 <HUA>
 A/Cross-references: GB:S40364; NID:g251668; PIDN:AA82554.2; PID:g5705957
 R/Huang, E.; Nocka, K.; Beier, D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Leder

Cell 63, 225-233, 1990
 A/Title: The hematopoietic growth factor K1 is encoded by the sl locus and is the ligand
 A/Reference number: A35976; MUID:91004221; PMID:1698557
 A/Accession: A35976

A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-206, 'S', 208-270 <HU2>
 A/Cross-references: GB:M38511

R/Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; March,
 Cell 63, 235-243, 1990
 A/Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active in

A/Reference number: A35977; MUID:91004223; PMID:1698558
 A/Accession: A35977
 A/Status: preliminary
 A/Molecule type: mRNA

A/Residues: 1-273 <AND>
 A/Cross-references: GB:M57647; GB:M38436; NID:g199151; PIDN:AAA39538.1; PID:g199152
 R/Copeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.O.; Jenkins, N.A.; Cosman, D.; An

Cell 63, 175-183, 1990
 A/Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and is
 A/Reference number: A35972; MUID:91004216; PMID:1698554
 A/Accession: A35972
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 26-53 <COP>
 A/Cross-references: GB:M59912
 R/Sebo, K.M.; Williams, D.A.; Geisler, E.N.; Brody, V.C.; Martin, F.H.; Atkins, H.L.;

; Catnach, B.M.; Galli, S.J.; Sugas, S.V.
 Cell 63, 213-224, 1990
 A:Title: Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for
 A:Reference number: A35975; MUID:91004220; PMID:1698556
 A:Accession: A35975
 A:Molecule type: mRNA
 A:Residues: 1-201 <25E>
 A:Cross-references: GB:M59915; NID:9200935; PIDN:AAA40095.1; PID:9554271
 R:Zeebo, K.M.; Wypych, J.; McNeice, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev,
 A: Langley, K.E.
 Cell 63, 195-201, 1990
 A:Title: Identification, purification, and biological characterization of hematopoietic
 A:Reference number: A35973; MUID:91004218; PMID:2208278
 A:Accession: A35973
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 21-29 'R', 31-39 <2S2>
 R:Brannan, C.I.; Bedell, M.A.; Resnick, J.L.; Eppig, J.J.; Handel, M.A.; Williams, D.E.;
 Genes Dev. 6, 1832-1842, 1992
 A:Title: Developmental abnormalities in Steel17H mice result from a splicing defect in
 A:Reference number: A44071; MUID:93012940; PMID:1383087
 A:Accession: I48768
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-206 'S', 208-273 <RES>
 A:Cross-references: EMBL:X68989; NID:9395283; PIDN:CAA48778.1; PID:9395284
 C:Genetics:
 A:Gene: SURF
 A:Map position: 10
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: extracellular protein; glycoprotein; transmembrane protein

Query Match 78.5%; Score 991; DB 2; Length 273;
 Best Local Similarity 72.2%; Pred. No. 5.6e-73;
 Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLFFNPLVKTGICRNRVTNNVQVTKLVANLPKQVMTTLKYVPG 60
 DB 1 MKKTQWTLTCTIYQLLFFNPLVKTGICRNRVTNNVQVTKLVANLPKQVMTTLKYVPG 60
 QY 61 MDVLPSCWISBENVVQLSDSLTDLDDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISBENVVQLSDSLTDLDDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENAP 120
 QY 121 KOLKSFSPKPERLFTPEPFRIFNRSIDAFKDFVVAASSETSDCVVSTLSPEK----- 174
 DB 121 KOLKSFSPKPERLFTPEPFRIFNRSIDAFKDFVVAASSETSDCVVSTLSPEKDSRVSVT 180
 QY 175 -----KAKNPQDSSLHMAAMALPALFSLIIGFAGALYWKRR 212
 DB 181 KPEMLPVAASSLRNDSNNRKAAPEDSGIQWTRMALPALISLVIGFAGALYWKRR 240
 QY 213 QPSLTRAVENTIQINEEDNEISMLQEKEREFQEV 245
 DB 241 QSSLTRAVENTIQINEEDNEISMLQEKEREFQEV 273

RESULT 8
 S58313
 stem cell factor precursor - sheep (fragment)
 C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
 C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
 C:Accession: S58313
 R:McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
 submitted to the EMBL Data Library, August 1995
 A:Description: Molecular cloning and biological activity of ovine stem cell factor.
 A:Reference number: S58313
 A:Accession: S58313
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-202 <MC1>
 A:Cross-references: EMBL:Z50743; NID:9940807; PIDN:CAA90620.1; PID:9940808
 C:Superfamily: mouse mast cell growth factor

Query Match 59.4%; Score 749.5; DB 2; Length 202;
 Best Local Similarity 83.9%; Pred. No. 1.5e-53;
 Matches 146; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLFFNPLVKTGICRNRVTNNVQVTKLVANLPKQVMTTLKYVPG 60
 DB 1 MKKTQWTLTCTIYQLLFFNPLVKTGICRNRVTNNVQVTKLVANLPKQVMTTLKYVPG 60
 QY 61 MDVLPSCWISBENVVQLSDSLTDLDDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISBENVVQLSDSLTDLDDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENHSF 120
 QY 121 KOLKSFSPKPERLFTPEPFRIFNRSIDAFKDFVVAASSETSDCVVSTLSPEK 173
 DB 121 KVVKSSKSPKPERLFTPEPFRIFNRSIDAFKDFVVAASSETSDCVVSTLSPEK 174

RESULT 9

stem cell factor protein precursor - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
 C:Accession: B35974; A39805
 R:Martin, F.H.; Sugas, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
 s, J.C.; Patel, A.C.; Fisher, E.F.; Enjavac, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, R
 Cell 63, 203-211, 1990
 A:Title: Primary structure and functional expression of rat and human stem cell factor D
 A:Reference number: A35974; MUID:91004219; PMID:2208279
 A:Accession: B35974
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-201 <MAR>
 A:Cross-references: GB:M59966; NID:9206861; PIDN:AAA42117.1; PID:9554507
 R:Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zeebo,
 A: Biol. Chem. 266, 8102-8107, 1991
 A:Title: Amino acid sequence and post-translational modification of stem cell factor iso
 A:Reference number: A39805; MUID:91217037; PMID:1708771
 A:Accession: A39805

A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 'E', 27-190 <LUA>
 C:Superfamily: mouse mast cell growth factor
 Query Match 57.1%; Score 721; DB 2; Length 201;
 Best Local Similarity 79.8%; Pred. No. 3e-51;
 Matches 138; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFFNPLVKTGICRNRVTNNVQVTKLVANLPKQVMTTLKYVPG 60
 DB 1 MKKTQWTLTCTIYQLLFFNPLVKTGICRNRVTNNVQVTKLVANLPKQVMTTLKYVPG 60
 QY 61 MDVLPSCWISBENVVQLSDSLTDLDDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISBENVVQLSDSLTDLDDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENAP 120
 QY 121 KOLKSFSPKPERLFTPEPFRIFNRSIDAFKDFVVAASSETSDCVVSTLSPEK 173
 DB 121 KVVKSLKPKPERLFTPEPFRIFNRSIDAFKDFVVAASSETSDCVVSTLSPEK 173

RESULT 10

stem cell factor short form precursor - quail
 C:Species: Coturnix coturnix (quail)
 C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
 C:Accession: S70367
 R:Petitje, J.N.; Kulik, M.J.
 Biochim. Biophys. Acta 1307, 149-151, 1996
 A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell fac
 A:Reference number: S70366; MUID:96283808; PMID:8679698
 A:Accession: S70367
 A:Molecule type: mRNA

A:Residues: 1-253 <PET>
 A:Cross-references: EMBL:U43079; NID:g1150877; PIDN:AAC59934.1; PID:g1150878
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: growth factor; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-253/Product: stem cell factor short form #status predicted <MAT>
 F:192-216/Domain: transmembrane #status predicted <TM>

Query Match 47.9%; Score 605; DB 2; Length 253;
 Best Local Similarity 49.8%; Pred. No. 1e-41; 71; Indels 8; Gaps 5;
 Matches 126; Conservative 46; Mismatches 71; Indels 8; Gaps 5;

QY 1 MKKTQWIIITCIIYQLLEFNPVKTGICRNVYNNVQVTKLVANLPKDYMITLKXVVG 60
 1 MKKAQWIIITCFCIQLLINPLVKTQSSCGNPPTDVNDIAKLVGNLPNDYILITLKXVPG 60
 DB 61 MDVLPSCWISSENVQVLSLTLDKF--SNISGLSNYSIITDKLVNIVDLVCEVKE 117
 61 MDSLPHNCWHLMWPEFSRSLHNLLQKFVDSIDMSDVLSNYSIINNLTIRIINDLMACLA 120
 QY 118 NSSKD-LKKSFKSPPEPLFTPEEPFRIPNRSIDAFKDFVVASSTDCVVSSTL-SPEK 175
 121 DNKKDPIKENGHLIYEDRPIENPFRLNRTILEVKEFADSLDKNDCTIMPSTVETPE 180
 DB 176 AKNPPGDSLSHMAAMLPALFSLIIGFAGALYMKKROP-SLTRAVENTIQIN--EEDNEI 232
 181 ALGFSSSSLOGISIALTSLSLIGFIIIGVITMKTHPKSRPESNETTQCHGQENEL 240
 QY 233 SMLQEKREPEOV 245
 241 SMLQEKREHLQV 253
 DB

RESULT 11

JN0637
 stem cell factor precursor - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jul-2000
 C:Accession: JN0637
 R:Zhou, J.H.; Ohkaki, M.; Sakurai, M.
 Gene 127, 269-270, 1993
 A:Title: Sequence of a cDNA encoding chicken stem cell factor.
 A:Reference number: JN0637; MID:93273244; PMID:7684722
 A:Accession: JN0637
 A:Molecule type: mRNA
 A:Residues: 1-287 <ZHO>
 A:Cross-references: GB:D13516; NID:g931648; PIDN:BA02733.1; PID:g931649
 A:Experimental source: brain
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: growth factor; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-287/Product: stem cell factor #status predicted <MAT>
 F:226-248/Domain: transmembrane #status predicted <TM>

Query Match 46.3%; Score 584; DB 2; Length 287;
 Best Local Similarity 44.6%; Pred. No. 6.2e-40;

Matches 128; Conservative 46; Mismatches 71; Indels 42; Gaps 7;
 QY 1 MKKTQWIIITCIIYQLLEFNPVKTGICRNVYNNVQVTKLVANLPKDYMITLKXVVG 60
 1 MKKAQWIIITCFCIQLLINPLVKAQSSCGNPPTDVNDIAKLVGNLPNDYILITLKXVPG 60
 DB 61 MDVLPSCWISSENVQVLSLTLDKF--SNISGLSNYSIITDKLVNIVDLVCEVKE 117
 61 MDSLPHNCWHLMWPEFSRSLHNLLQKFSDISMSDVLSNYSIINNLTIRIINDLMACLA 120
 QY 118 NSSKD-LKKSFKSPPEPLFTPEEPFRIPNRSIDAFKDFVVASSTDCVVSSTL-SPEK 175
 121 DNKKDPIKENGHLIYEDRPIENPFRLNRTILEVKEFADSLDKNDCTIMPSTVETPE 180
 DB 176 AKNPPGDSLSHMAAMLPALFSLIIGFAGALYMKKROP-SLTRAVENTIQIN--EEDNEI 232
 181 ALGFSSSSLOGISIALTSLSLIGFIIIGVITMKTHPKSRPESNETTQCHGQENEL 240
 QY 233 SMLQEKREPEOV 245
 241 SMLQEKREHLQV 253
 DB

QY 202 FAFGALYMKKROP-SLTRAVENTIQIN--EEDNEISMLQEKREPEOV 245
 241 FILGALYMKKTHPKSRPESNETTQCHGQENELSMLOQKEKHLQV 287
 DB

RESULT 12

S70366
 stem cell factor long form precursor - quail
 C:Species: Coturnix coturnix (quail)
 C>Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
 C:Accession: S70366
 R:Petitje, J.N.; Kulik, M.J.
 Biochim. Biophys. Acta 1307, 149-151, 1996
 A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell fac
 A:Reference number: S70366; MID:96283808; PMID:8679698
 A:Accession: S70366
 A:Molecule type: mRNA
 A:Residues: 1-287 <PET>
 A:Cross-references: EMBL:U43078; NID:g1150875; PIDN:AAC59933.1; PID:g1150876
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: growth factor; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-287/Product: stem cell factor long form #status predicted <MAT>
 F:226-250/Domain: transmembrane #status predicted <TM>

Query Match 46.2%; Score 583; DB 2; Length 287;
 Best Local Similarity 44.3%; Pred. No. 7.4e-40;

Matches 127; Conservative 47; Mismatches 71; Indels 42; Gaps 7;
 QY 1 MKKTQWIIITCIIYQLLEFNPVKTGICRNVYNNVQVTKLVANLPKDYMITLKXVVG 60
 1 MKKAQWIIITCFCIQLLINPLVKTQSSCGNPPTDVNDIAKLVGNLPNDYILITLKXVPG 60
 DB 61 MDVLPSCWISSENVQVLSLTLDKF--SNISGLSNYSIITDKLVNIVDLVCEVKE 117
 61 MDSLPHNCWHLMWPEFSRSLHNLLQKFVDSIDMSDVLSNYSIINNLTIRIINDLMACLA 120
 QY 118 NSSKD-LKKSFKSPPEPLFTPEEPFRIPNRSIDAFKDFVVASSTDCVVSSTL-SPEK 175
 121 DNKKDPIKENGHLIYEDRPIENPFRLNRTILEVKEFADSLDKNDCTIMPSTVETPE 180
 DB 176 AKNPPGDSLSHMAAMLPALFSLIIGFAGALYMKKROP-SLTRAVENTIQIN--EEDNEI 232
 181 ALGFSSSSLOGISIALTSLSLIGFIIIGVITMKTHPKSRPESNETTQCHGQENEL 240
 QY 202 FAFGALYMKKROP-SLTRAVENTIQIN--EEDNEISMLQEKREPEOV 245
 241 FILGALYMKKTHPKSRPESNETTQCHGQENELSMLOQKEKHLQV 287
 DB

RESULT 13

S29052
 stem cell factor - human (fragments)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: S29052
 R:Lu, H.S.; Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderak, K.; Baltera J
 Arch. Biochem. Biophys. 298, 150-158, 1992
 A:Title: Post-translational processing of membrane-associated recombinant human stem cell
 A:Reference number: S29052; MID:92398336; PMID:1381905
 A:Accession: S29052
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
 C:Superfamily: mouse mast cell growth factor

Query Match 38.9%; Score 491.5; DB 2; Length 124;
 Best Local Similarity 72.3%; Pred. No. 6.6e-33;
 Matches 107; Conservative 0; Mismatches 41; Indels 4;

QY 26 EGICRNVYNNVQVTKLVANLPKDYMITLKXVPGMDVLPSCWISSENVQVLSLTL 85

```

Db      1  EGIICRRNTNNVK-----DVLPSHCWISSEWVQLS----- 30
QY      86  DKFSNTSEGLSNYSIIDKLVNIIVDLVECKENSSKDLKSKFSPPEPRLFTPEEPFRIN 145
Db      31  DKFSNTSEGLSNYSII-----DDLVECKENSSKDLKSKFSPPEPRLFTPEEPFRIN 83
QY      146  RSIDAFKDFVVASETSDCVVSTLSPEK 173
Db      84  RSI----DFVVASETSDCVVSTLSPEK 107

```

RESULT 14

```

B35971
mast cell growth factor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: B35971
R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I
Cell 63, 167-174, 1990
A:Title: Identification of a ligand for the c-kit proto-oncogene.
A:Reference number: A35971; MUID:91004215; PMID:1698553
A:Accession: B35971
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-51 <WIL>
C:Superfamily: mouse mast cell growth factor
C:Keywords: transmembrane protein

```

```

Query Match      13.9%; Score 175.5; DB 2; Length 51;
Best Local Similarity 72.3%; Pred. No. 9e-08;
Matches 34; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

```

```

QY      28  ICRNRVTNNVKDITKLVANLPKDYMITLKVPKGMVLPKSHCWISENV 74
Db      3  ICGNPVTNVDKITKLVANLPNDYMITLVNAGMDVLPK-WMLDDMI 48

```

RESULT 15

```

A35971
mast cell growth factor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: A35971
R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I
Cell 63, 167-174, 1990
A:Title: Identification of a ligand for the c-kit proto-oncogene.
A:Reference number: A35971; MUID:91004215; PMID:1698553
A:Accession: A35971
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-49 <WIL>
C:Superfamily: mouse mast cell growth factor
C:Keywords: transmembrane protein

```

```

Query Match      13.7%; Score 172.5; DB 2; Length 49;
Best Local Similarity 73.5%; Pred. No. 1.5e-07;
Matches 36; Conservative 4; Mismatches 6; Indels 3; Gaps 2;

```

```

QY      28  ICRNRVTNNVKDITKLVANLPKDYMITLKVPKGMVLPKSHCWISENVQ 76
Db      3  ICGNPVTNVDKITKLVANLPNDYMITLVNAGMDVLPK-WY-DWVIQ 48

```

Search completed: February 5, 2004, 15:08:22
Job time : 14.8361 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:42:38 ; Search time 7.76171 Seconds
(without alignments)
1484.408 Million cell updates/sec

Title: US-09-224-683-63

Perfect score: 1262

Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISWLQEKEREPQEV 245

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1231	97.5	273	1 SCF_HUMAN	P21583 homo sapien
2	1053.5	83.5	274	1 SCF_HORSE	Q95md2 equus caball
3	1051.5	83.3	274	1 SCF_FELCA	P79169 felis silve
4	1037.5	82.2	274	1 SCF_PIG	Q29030 sus scrofa
5	1021.5	80.9	274	1 SCF_CARI	Q95m19 capra hircu
6	1018.5	80.7	274	1 SCF_BOVIN	Q28132 bos taurus
7	1014.5	80.4	274	1 SCF_CANFA	Q06220 canis famli
8	1014.5	80.4	274	1 SCF_MUSVI	Q95n18 mustela vis
9	992	78.6	273	1 SCF_RAT	P21581 rattus norv
10	991	78.5	273	1 SCF_MOUSE	P20826 mus musculu
11	990.5	78.5	267	1 SCF_SHEEP	P79368 ovis aries
12	584	46.3	287	1 SCF_CHICK	Q09108 gallus gall
13	583	46.2	287	1 SCF_COTUA	Q08214 coturnix co
14	99	7.8	496	1 MURE_WIGBR	Q84211 wigglewort
15	97	7.7	482	1 T2BA_YEAST	P36100 saccharomyc
16	94.5	7.5	403	1 RAGE_MOUSE	Q62151 mus musculu
17	91	7.2	378	1 FDHA_METUA	Q60314 methanococc
18	91	7.2	402	1 RAGE_RAT	Q63495 rattus norv
19	91	7.2	981	1 SC44_RICFE	Q9a137 rickettsia
20	90.5	7.2	1675	1 POL_RTBVP	P27502 rickettsia
21	90	7.1	267	1 PK1_NPVHZ	P41719 heliothis z
22	90	7.1	411	1 RMUC_CHUPN	Q92687 chlamydia p
23	90	7.1	1039	1 PDP2_ARATH	Q9m968 arabidopsis
24	89	7.1	2238	1 RRP1_BUNYW	P20470 bunyameera
25	88	7.0	447	1 DNAA_SYNY3	P49955 synecocyst
26	87.5	6.9	966	1 SRS2_YEAST	Q02715 medicago sa
27	87.5	6.9	1175	1 SRS2_YEAST	P27954 saccharomyc
28	87.5	6.9	1813	1 UN13_CAREL	P27175 caenorhabdi
29	87	6.9	664	1 ZAAA_CAREL	Q09543 caenorhabdi
30	86.5	6.9	384	1 NRFF_HABIN	P44942 haemophilus
31	86.5	6.9	2492	1 TALA_DICDI	P54633 dictyostell
32	86	6.8	469	1 C39A_HUMAN	Q9ny15 homo sapien
33	86	6.8	1146	1 KMHA_DICDI	P42557 dictyostell

34	85	6.7	805	1 SUS2_ARATH	Q00917 arabidopsis
35	85	6.7	953	1 UVRA_RICPR	Q9zcc3 rickettsia
36	85	6.7	1188	1 PSRA_METUA	Q32962 methanococc
37	84.5	6.7	466	1 DNAA_PROMT	P22837 proteus mir
38	84.5	6.7	964	1 CAP2_TOBAC	P27154 nicotiana t
39	84.5	6.7	1075	1 PST2_SCHPO	Q13919 schizosacch
40	84.5	6.7	2156	1 RPI_HUMAN	P56715 homo sapien
41	84	6.7	935	1 COBG_YEAST	P32074 saccharomyc
42	84	6.7	935	1 YJ31_YEAST	P40355 saccharomyc
43	84	6.7	1224	1 YGNS_YEAST	P52918 saccharomyc
44	84	6.7	1522	1 BA13_HUMAN	Q60242 homo sapien
45	83.5	6.6	442	1 MURC_STRPB	Q8p2el streptococc

ALIGNMENTS

RESULT 1
ID SCF_HUMAN STANDARD; PRT; 273 AA.
AC P21583; Q16487; Q9UOK7;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG OR MGF OR SCF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1)
RX MEDLINE=91004219; PubMed=2208279;
RA Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
RA Morris C.F., McNeice I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
RA Smith K.A., Johnson M.U., Flores J.C., Patel A.C.,
RA Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,
RA Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zeebo K.M.,
RT "Primary structure and functional expression of rat and human stem
RT cell factor DNAs."
RL Cell 63:203-211(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2)
RX MEDLINE=9160429; PubMed=10049787;
RA Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.,
RT "Parathyroid hormone-regulated production of stem cell factor in human
RT osteoblasts and osteoblast-like cells."
RL Biochem. Biophys. Res. Commun. 255:778-784(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Han C., Peng X., Yuan J., Qiang B.,
RN Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 167-248 FROM N.A. (ISOFORM 2).
RX MEDLINE=92360843; PubMed=1379846;
RA Toyota M., Hinoeda Y., Itoh F., Tsujisaki M., Inai K., Yachi A.,
RT "Expression of two types of kit ligand mRNAs in human tumor cells."
RL Int. J. Hematol. 55:301-304(1992).
RN [5]
RP FUNCTION: Stimulates the proliferation of both myeloid and lymphoid
RP augment the proliferation of both myeloid and lymphoid
RP hematopoietic progenitors in bone marrow culture. Mediates also
RP cell-cell adhesion. Acts synergistically with other cytokines,
RP probably interleukins.
CC -! SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -! SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
CC Also exists as a secreted soluble form (isoform 1 only) (By
CC similarity).
CC -! ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=SCF248;
CC IsoId=P21583-1; Sequence=Displayed;
CC Name=2; Synonyms=SCF220;

```

CC      IsoId=215163-2; Sequence=VSP_006022;
CC      DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC      -!- PTM: A soluble form is produced by proteolytic processing of
CC      isoform 1 in the extracellular domain.
CC      -!- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC      -!- DATABASE: NAME=Atlas Genet. Cytoenet. Oncocol. Haematol.;
CC      WWW="http://www.intobioigen.fr/services/chromosome/Genes/MGFD142.html"
CC
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CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; M59964; AAA85450.1; -
CC      DR      EMBL; AF119835; AAD22048.1; -
CC      DR      EMBL; AF400436; AAK92485.1; -
CC      DR      EMBL; AF400437; AAK92486.1; -
CC      DR      EMBL; S42571; AAB22846.2; -
CC      DR      PIR; A35974; A35974.
CC      DR      PIR; B61190; B61190.
CC      DR      Genew; HGNC:6343; KITLG.
CC      MIM; 184745; -
CC      DR      GO; 0005173; P:stem cell factor receptor binding activity; TAS.
CC      DR      GO; 0008283; P:cell proliferation; TAS.
CC      DR      GO; 0007165; P:signal transduction; TAS.
CC      DR      InterPro; IPR003452; SCF.
CC      DR      Pfam; PF02404; SCF.1.
CC      KW      Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
CC      KW      Alternative splicing.
CC      FT      SIGNAL 1 25
CC      FT      CHAIN 26 273
CC      FT      DOMAIN 26 214
CC      FT      TRANSMEM 215 237
CC      FT      DOMAIN 238 273
CC      FT      DISULFD 29 114
CC      FT      DISULFD 68 163
CC      FT      CARBOHYD 90 90
CC      FT      CARBOHYD 97 97
CC      FT      CARBOHYD 118 118
CC      FT      CARBOHYD 145 145
CC      FT      CARBOHYD 195 195
CC      FT      VARSPLIC 174 202
CC
CC      KIT LIGAND.
CC      EXTRACELLULAR (POTENTIAL).
CC      POTENTIAL.
CC      CYTOPLASMIC (POTENTIAL).
CC      BY SIMILARITY.
CC      BY SIMILARITY.
CC      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      DSRVSTKPEMLPPVAASSLRDNSSSNR -> G (in
CC      isoform 2).
CC      FTRID=VSP_006022.
CC      L -> S (IN REF. 2 AND 3; AAK92486).
CC      K -> R (IN REF. 2 AND 3; AAK92486).
CC      L -> F (IN REF. 2 AND 3; AAK92486).
CC
CC      SEQUENCE 273 AA; 30898 MW; 19FD32CB59C607 CRC64;
CC
CC      Query Match 97.5%; Score 1231; DB 1; Length 273;
CC      Best Local Similarity 89.4%; Pred. No. 8 6e-91;
CC      Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
CC
CC      1 MKKTQWILTCIYLQLLFNPLVKTGICRNVYNNVKDVKLVANLPKDYMITLKAYPG 60
CC      Db 1 MKKTQWILTCIYLQLLFNPLVKTGICRNVYNNVKDVKLVANLPKDYMITLKAYPG 60
CC
CC      61 MDVLPBSHCWISSEWVQJSDSLTDLLDKFSNISGSLNSYIIDLKLVNIYDDLVECYKENS 120
CC      Db 61 MDVLPBSHCWISSEWVQJSDSLTDLLDKFSNISGSLNSYIIDLKLVNIYDDLVECYKENS 120
CC
CC      121 KDLKKSFKSPSPRLFPPEEFRLFNDSIDAFKQFVAASSTSCVSSSTLSPKDSRVST 174
CC      Db 121 KDLKKSFKSPSPRLFPPEEFRLFNDSIDAFKQFVAASSTSCVSSSTLSPKDSRVST 174
CC
CC      121 KDLKKSFKSPSPRLFPPEEFRLFNDSIDAFKQFVAASSTSCVSSSTLSPKDSRVST 180
CC      Db 121 KDLKKSFKSPSPRLFPPEEFRLFNDSIDAFKQFVAASSTSCVSSSTLSPKDSRVST 180
CC
CC      175 -----AKNPQGDSSLHMAAMLPALFSILIGFAGALYMKKR 212
CC      Db 181 KPFWLPPEVAASSLRNSSSSSRKAKNPQGDSSLHMAAMLPALFSILIGFAGALYMKKR 240
CC      213 QPSLTRAVENTIQINEEDNEISMLQEKREBFQEV 245

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Db      241  QPSLTRAVENTIQINEDNEISMLOEKERFQEV 273
RESULT 2
SCF_HORSE
ID      SCF_HORSE      STANDARD:      PRT: 274 AA.
AC      095MD2: 062765; 095MG7; 095MG8; 09N1Y5;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE      cell growth factor) (MGF).
DE      KITLG OR MGF OR SCF.
OS      Equus caballus (Horse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
CX      NCBI_TaxID=9796;
RN      [1]
RP      SEQUENCE OF 4-264 FROM N.A.
RA      Terry R.R., Mickelson J.R., Schmutz S., Cochran E.G., Bailey E.;
RT      "Equus caballus mast cell growth factor (MGF).";
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE OF 12-267 FROM N.A.
RA      Riuder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
RT      "An Equine sequence homologous to stem cell factor (KIT-ligand).";
RL      Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE OF 107-202 AND 227-274 FROM N.A.
RA      Terry R.R., Bailey E.F., Cochran E.G.;
RT      "Evaluation of MGF as the candidate gene for Appaloosa spotting.";
RL      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE OF 147-197 FROM N.A.
RA      Caetano A.R., Shihue Y.-L., Lyons L.A., Laughlin T.F., O'Brien S.J.,
RA      Murray J.D., Bowling A.T.;
RT      "A primary Human-Horse comparative gene map.";
RL      Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC      -I- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC      augment the proliferation of both myeloid and lymphoid
CC      hematopoietic progenitors in bone marrow culture. Mediates also
CC      cell-cell adhesion. Acts synergistically with other cytokines,
CC      probably interleukins (By similarity).
CC      -I- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC      -I- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
CC      secreted soluble form (By similarity).
CC      -I- PFM: A soluble form is produced by proteolytic processing of
CC      the extracellular domain (By similarity).
CC      -I- SIMILARITY: BELONGS TO THE SCF FAMILY.
-----
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CC      the European Bioinformatics Institute. There are no restrictions on ways
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.ebi-sib.ch/announce/
CC      or send an email to license@ebi-sib.ch).
-----
CC      EMBL; AF401625; AAK94474.1; -
CC      EMBL; AF053498; AAC97076.1; -
CC      EMBL; AF677704; AAK63249.1; -
CC      EMBL; AF367706; AAK63250.1; -
CC      EMBL; AF130770; AAK63276.1; -
CC      EMBL; AF130770; AAK63276.1; -
CC      InterPro; IPR003452; SCF.
CC      Pfam; PF02404; SCF. 1.
CC      Growth factor; Glycoprotein; Transmembrane; signal; Cell adhesion.
CC      SIGNAL 1 25 POTENTIAL.
CC      CHAIN 26 274 KIT LIGAND.
CC      DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
CC      TRANSMEM 216 238 POTENTIAL.
CC      CYTOPLASMIC 239 274 POTENTIAL.

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FT DISULFID 29 114 BY SIMILARITY.
 FT DISULFID 68 164 BY SIMILARITY.
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 15 15 Q -> P (IN REF. 2).
 FT CONFLICT 241 241 MISSING (IN REF. 3).
 SQ SEQUENCE 274 AA; 31217 MW; 96C1D4C9059132F2 CRC64;

Query Match 83.5%; Score 1053.5; DB 1; Length 274;
 Best Local Similarity 76.6%; Pred. No. 1.1e-76;
 Matches 210; Conservative 19; Mismatches 16; Indels 29; Gaps 2;

QY 1 MKKTQWILTCIYDQLLFPNPLVKTGICRNRTNNVQVTLVNLPRDVMITLKYVPG 60
 DB 1 MKKTQWILTCIYDQLLFPNPLVKTGICRNRTNNVQVTLVNLPRDVMITLKYVPG 60
 QY 61 MDVLPSCWISWVQVLSLTDLPKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISWVQVLSLTDLPKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDF-VVASETSDCVVSTLSPEKG----- 174
 DB 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDF-VVASETSDCVVSTLSPEKG----- 174
 QY 121 ENVKKSKYKQESRLFTPEEFPRIFNRSIDAFKDFLEWVSKTSCVVSSTLSPEKDSRVSV 180
 DB 121 ENVKKSKYKQESRLFTPEEFPRIFNRSIDAFKDFLEWVSKTSCVVSSTLSPEKDSRVSV 180
 QY 175 -----KAKNPPGDSLHMAAMALPALFSLIIGFAFGALYMKK 211
 DB 181 TKPFMLPVAASLSLRNDSSSNRKASNFTGDSNLMQAMMALPAFSLVIGFAFGALYMKK 240
 QY 212 ROPSLTRAVENTIINEEDNEISMLOEKERPEQEV 245
 DB 241 KQPNLTRAVENIINEEDNEISMLOEKERPEQEV 274

RESULT 3
 SCF FELCA STANDARD; PRT; 274 AA.
 ID - SCF FELCA STANDARD; PRT; 274 AA.
 AC F79169;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
 GN KITLG OR SCF.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA MEDLINE=97069946; PubMed=8912926;
 RT Dunham S.P., Orlions D.E.;
 RT "The cloning and sequencing of cDNAs encoding two isoforms of feline stem cell factor".
 RL DNA Seq. 6:233-237(1996).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2). Also exists as a secreted soluble form (isoform 1 only) (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC Name=2;
 CC IsoId=P79169-1; Sequence=Displayed;
 CC IsoId=P79169-2; Sequence=VSP 006021;
 CC -1- PTM: A soluble form is produced by proteolytic processing of

CC isoform 1 in the extracellular domain (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 CC EMBL; D50833; BAA09445.1; -.
 CC InterPro; IPR003452; SCF.
 DR Pfam; PF02404; SCF; 1.
 DR Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
 KW Alternative splicing.
 FT SIGNAL 1 25
 FT CHAIN 26 274
 FT DOMAIN 26 215
 FT TRANSMEM 216 238
 FT DOMAIN 239 274
 FT DISULFID 29 114
 FT DISULFID 68 164
 FT CARBOHYD 90 90
 FT CARBOHYD 97 97
 FT CARBOHYD 145 145
 FT CARBOHYD 196 196
 FT CARBOHYD 203 203
 FT VARSPLIC 175
 FT FTId=VSP 006021.
 SQ SEQUENCE 274 AA; 30987 MW; C5B78DB4791237BE CRC64;

Query Match 83.3%; Score 1051.5; DB 1; Length 274;
 Best Local Similarity 76.6%; Pred. No. 1.1e-76;
 Matches 210; Conservative 17; Mismatches 18; Indels 29; Gaps 2;

QY 1 MKKTQWILTCIYDQLLFPNPLVKTGICRNRTNNVQVTLVNLPRDVMITLKYVPG 60
 DB 1 MKKTQWILTCIYDQLLFPNPLVKTGICRNRTNNVQVTLVNLPRDVMITLKYVPG 60
 QY 61 MDVLPSCWISWVQVLSLTDLPKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISWVQVLSLTDLPKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDF-VVASETSDCVVSTLSPEKG----- 174
 DB 121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDF-VVASETSDCVVSTLSPEKG----- 174
 QY 121 ENVKKSKYKQESRLFTPEEFPRIFNRSIDAFKDFLEWVSKTSCVVSSTLSPEKDSRVSV 180
 DB 121 ENVKKSKYKQESRLFTPEEFPRIFNRSIDAFKDFLEWVSKTSCVVSSTLSPEKDSRVSV 180
 QY 175 -----KAKNPPGDSLHMAAMALPALFSLIIGFAFGALYMKK 211
 DB 181 TKPFMLPVAASLSLRNDSSSNRKATNPIDESSIQAMMALPACRSLVIGFAFGALYMKK 240
 QY 212 ROPSLTRAVENTIINEEDNEISMLOEKERPEQEV 245
 DB 241 KQPNLTRAVENIINEEDNEISMLOEKERPEQEV 274

RESULT 4
 SCF PIG STANDARD; PRT; 274 AA.
 ID - SCF PIG STANDARD; PRT; 274 AA.
 AC Q29030;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
 GN KITLG OR MGF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;
 RX MEDLINE=94146218; PubMed=7508758;
 RA Zhang Z., Anthony R.V.;
 RT "porine stem cell factor/C-kit ligand: its molecular cloning and
 localization within the uterus.";
 RL Eiol. Reprod. 50:95-102(1994).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 augment the proliferation of both myeloid and lymphoid
 hematopoietic progenitors in bone marrow culture. Mediates also
 cell-cell adhesion. Acts synergistically with other cytokines,
 probably interleukins (By similarity).
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
 secreted soluble form (By similarity).
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 the extracellular domain (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L07786; AAA53670.1; -.
 DR PIR; I46575; I46575.
 DR InterPro; IPR003452; SCF.1.
 DR Pfam; PF02404; SCF.1.
 KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 FT SIGNAL 1 25
 FT CHAIN 26 274
 FT DOMAIN 26 215
 FT TRANSMEM 216 238
 FT DISULFID 29 114
 FT CARBOHYD 68 164
 FT CARBOHYD 90 90
 FT CARBOHYD 97 97
 FT CARBOHYD 145 145
 FT CARBOHYD 196 196
 FT CARBOHYD 3118 MM; FF3C87114D7BA6A6 CRC64;
 SQ SEQUENCE 274 AA; 3118 MM; FF3C87114D7BA6A6 CRC64;

 Query Match 82.2%; Score 1037.5; DB 1; Length 274;
 Best Local Similarity 75.2%; Pred. No. 2e-75;
 Matches 206; Conservative 22; Mismatches 17; Indels 29; Gaps 2;

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast
 cell growth factor) (MGF).
 GN KITLG OR SCF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OK NCBI_TaxID=9925;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Shiba; TISSUE=Brain;
 RA Yanagisawa N., Tanaka S., Yamamouchi K., Tojo H., Tachi C.;
 RT "Identification of splicing isoforms of caprine stem cell factor
 (GSCF) transcripts and expression patterns of the two major isoforms,
 gSCF825 and gSCF741, in the brain and the skin of adult and fetal
 RT Shiba goats, Capra hircus";
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 augment the proliferation of both myeloid and lymphoid
 hematopoietic progenitors in bone marrow culture. Mediates also
 cell-cell adhesion. Acts synergistically with other cytokines,
 probably interleukins (By similarity).
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
 secreted soluble form (By similarity).
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 the extracellular domain (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB002152; BAB71753.1; -.
 DR InterPro; IPR003452; SCF.1.
 DR Pfam; PF02404; SCF.1.
 KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 FT SIGNAL 1 25
 FT CHAIN 26 274
 FT DOMAIN 26 215
 FT TRANSMEM 216 238
 FT DISULFID 29 114
 FT CARBOHYD 68 164
 FT CARBOHYD 90 90
 FT CARBOHYD 97 97
 FT CARBOHYD 145 145
 FT CARBOHYD 196 196
 FT CARBOHYD 31052 MM; BBFE69A509EF65D CRC64;
 SQ SEQUENCE 274 AA; 31052 MM; BBFE69A509EF65D CRC64;

 Query Match 80.9%; Score 1021.5; DB 1; Length 274;
 Best Local Similarity 74.5%; Pred. No. 3.8e-74;
 Matches 204; Conservative 20; Mismatches 21; Indels 29; Gaps 2;

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Oy 175-----KXNPGPGSLHWMAAMALPALFSLILGAFALTYWK 211
Db 181 TKPFLPPVYAASSLNDSSSNRRKASNIEDSSLOMAAVALPAPFLVIGFAPALTYWK 240
Oy 212 RQPSLTRAVENTIQTINEEDNEISMLOEKREFOEV 245
Db 241 KQPNLTRTVENRQINEEDNEISMLOEKREFOEV 274

RESULT 6
SCF_BOVIN STANDARD; PRT; 274 AA.
ID SCF_BOVIN Q28132; O9TU74;
AC Q28132; O9TU74;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG OR SCF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Spleen;
RX MEDLINE=94339176; PubMed=7520283;
RA Zhou J., Hikono H., Ohnaki M., Kubota T., Sakurai M.;
RT "Cloning and characterization of cDNAs encoding two normal isoforms of
RL bovine stem cell factor.";
RN Biochim. Biophys. Acta 1223:148-150(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal brain;
RA Kudo T.;
RT "Bovine counterpart of stem cell factor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 204-239 FROM N.A., AND VARIANT ASP-218.
RC STRAIN=Belgian Blue;
RX MEDLINE=99315331; PubMed=10384045;
RA Seltz J.J., Schmutz S.M., Thue T.D., Buchanan F.C.;
RT "A missense mutation in the bovine MGF gene is associated with the
RL roan phenotype in Belgian Blue and Shorthorn cattle.";
RN Mamm. Genome 10:710-712(1999).
CC -!- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -!- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
CC Also exists as a secreted soluble form (isoform 1 only) (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC Name=2;
CC IsoId=Q28132-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q28132-2; Sequence=VSP_006020;
CC -!- PTM: A soluble form is produced by proteolytic processing of
CC isoform 1 in the extracellular domain (By similarity).
CC -!- POLYMORPHISM: The Roan locus is responsible for the coat
CC coloration of Belgian Blue and Shorthorn cattle. The solid-colored
CC and white animals are homozygotes, and the roan animals, with
CC intermingled colored and white hairs, are heterozygous. The roan
CC phenotype is due to the Asp-218 mutation.
CC -!- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC -----
DR EMBL; D28934; BAA06061.1; -.
DR EMBL; AB033716; BAA94808.1; -.
DR EMBL; AF120154; AAD55355.1; -.
DR PIR; S47571; S47571.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW Alternative splicing; Polymorphism.
KW SIGNAL
FT CHAIN
FT SIGNAL 1 25
FT CHAIN 26 274
FT DOMAIN 26 215
FT TRANSMEM 216 238
FT DOMAIN 239 274
FT DISULFID 29 114
FT DISULFID 68 164
FT CARBOHYD 90 90
FT CARBOHYD 145 145
FT CARBOHYD 196 196
FT VARSPLIC 175 203
FT
FT
FT VARIANT 218 218
SQ SEQUENCE 274 AA; 31014 MW; D6CIDDB77B0CB12B CRC64;
Query Match 80.7%; Score 1018.5; DB 1; Length 274;
Best local similarity 74.1%; Pred. No. 6.6e-74;
Matches 203; Conservative 20; Mismatches 22; Indels 29; Gaps 2;
QY 1 MKKTQTMILTCIYQLLLFNPLVTEGICENRNVYNNKVDYTKLVANPKDYMITLKYVPG 60
DB 1 MKKTQTMILTCIYQLLLFNPLVHTGQICENRNVYDDYKDYTKLVANPKDYMITLKYVPG 60
QY 61 MDVLPSSHCHWISSEWVQVQSDSLTDLDFKSNISSEGLSNYSIIDKLNVIVDDLVECVKENSS 120
DB 61 MDVLPSSHCHWISSEWVQVQSDSLTDLDFKSNISSEGLSNYSIIDKLNVIVDDLVECVKENSS 120
QY 121 KDLKKSFKSPDEPRFLFTPEBEFFRIFNKRISDAFCDF -VVASETSQCVASTISPEKGG----- 174
DB 121 ENVKKSSKSPDEPRQFTPEKFFGIFNKSIDAFKOLEIVASIKMSBCVSISSSTSPKDSRSVY 180
QY 121 KAKKPPDSSLSHMAAMALPLFLSLIGFAFGALYMKK 211
DB 181 TKRPMLPVPVAAASSLRNDSSSSNRKAASISIDSSLSQMAAYVALPAFFSLVIGFAFGAFYMKK 240
QY 212 RQPSLTRAVENTQINEEDNEISMLQEKEREFOEY 245
DB 241 KQPSLTRAVENTQINEEDNEISMLQEKEREFOEY 274
RESULT 7
SCF_CANFA STANDARD; PRT; 274 AA.
AC 006220; OSBPM6;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
cell growth factor) (MGF).
GN KITLG OR MGF
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=93106145; PubMed=1281786;
RA Shull R.M., Sugess S.V., Langley K.E., Okino K.H., Jacobsen F.W.,

```

Query Match	Best Local Similarity	Matches 205;	Conservative 17;	Mismatches 23;	Indels 29;	Gaps 2;
80.4%; Score 1014.5; DB 1; Length 274;	74.8%; Pred. No. 1.4e-73;					
1 MKKTQWTWLTCTIYIQLLFFNLVLTKEGICRRRVYNNVNDYTKLVANLPKDYMTILTKYVP 60	1 MKKTQWTWLTCTIYIQLLFFNLVLTKEGICRRRVYNNVNDYTKLVANLPKDYMTILTKYVP 60					
1 MKKTQWTWLTCTIYIQLLFFNLVLTKEGICRRRVYNNVNDYTKLVANLPKDYMTILTKYVP 60	1 MKKTQWTWLTCTIYIQLLFFNLVLTKEGICRRRVYNNVNDYTKLVANLPKDYMTILTKYVP 60					
61 MDVLPSCWISSEMYVQVSDSLTDLDDKPSNTSEGLSNYSIIDKLVINYVDLVEVCXENSS 120	61 MDVLPSCWISSEMYVQVSDSLTDLDDKPSNTSEGLSNYSIIDKLVINYVDLVEVCXENSS 120					
61 MDVLPSCWISSEMYVQVSDSLTDLDDKPSNTSEGLSNYSIIDKLVINYVDLVEVCXENSS 120	61 MDVLPSCWISSEMYVQVSDSLTDLDDKPSNTSEGLSNYSIIDKLVINYVDLVEVCXENSS 120					
121 KDLKSPKSPBRLFTPEEPFRIFNRSIDAQKDF-VVASETSDCVVSSTLSPKXG----- 174	121 KDLKSPKSPBRLFTPEEPFRIFNRSIDAQKDF-VVASETSDCVVSSTLSPKXG----- 174					
121 KDLKSPKSPBRLFTPEEPFRIFNRSIDAQKDF-VVASETSDCVVSSTLSPKXG----- 174	121 KDLKSPKSPBRLFTPEEPFRIFNRSIDAQKDF-VVASETSDCVVSSTLSPKXG----- 174					
121 ENVKKAPELRLFTPEEPFRIFNRSIDAQKDF-VVASETSDCVVSSTLSPKXG----- 180	121 ENVKKAPELRLFTPEEPFRIFNRSIDAQKDF-VVASETSDCVVSSTLSPKXG----- 180					
121 ENVKKAPELRLFTPEEPFRIFNRSIDAQKDF-VVASETSDCVVSSTLSPKXG----- 180	121 ENVKKAPELRLFTPEEPFRIFNRSIDAQKDF-VVASETSDCVVSSTLSPKXG----- 180					
175 -----KAKNPGRGSSIHMAAMALPALPSLIGAFALYWK 211	175 -----KAKNPGRGSSIHMAAMALPALPSLIGAFALYWK 211					
175 -----KAKNPGRGSSIHMAAMALPALPSLIGAFALYWK 211	175 -----KAKNPGRGSSIHMAAMALPALPSLIGAFALYWK 211					
212 RQSLTRAVENIQTNEEDNETSMQEKREEROEV 245	212 RQSLTRAVENIQTNEEDNETSMQEKREEROEV 245					
212 RQSLTRAVENIQTNEEDNETSMQEKREEROEV 245	212 RQSLTRAVENIQTNEEDNETSMQEKREEROEV 245					
241 KQPNLTKRVENIQTNEEDNETSMQEKREEROEV 274	241 KQPNLTKRVENIQTNEEDNETSMQEKREEROEV 274					
241 KQPNLTKRVENIQTNEEDNETSMQEKREEROEV 274	241 KQPNLTKRVENIQTNEEDNETSMQEKREEROEV 274					

RESULT 9					
ID	_SCF_MUSVI	STANDARD:	PRT:	274 AA.	
AC	Q95N18; Q95NM5;				
DT	28-FEB-2003 (Rel. 41, Created)				
DR	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).				
GN	KITLG OR SCF.				
OS	Muscleta vison (American mink).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae; Mustela.				
OX	NCB1_TaxID=9667;				
RN	[1]				
RA	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RP	Bennett R.D., Murphy B.D.;				
RL	Submitted (NOV-2000)				
CC	- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).				
CC	- SUBUNIT: Homodimer, non-covalently linked (Probable).				
CC	- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).				
CC	- ALTERNATIVE PRODUCTS:				
CC	Event=Alternative splicing; Named isoforms=2;				
CC	Name=1;				
CC	IsoId=Q95N18-1; Sequence=Displayed;				
CC	Name=2;				
CC	IsoId=Q95N18-2; Sequence=VSP_006024;				
CC	- PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain (By similarity).				
CC	- SIMILARITY: BELONGS TO THE SCF FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/ or send an email to license@isb.ch).				
CC	-----				
DR	EMBL; AY013712; AACG7434.1; -				
DR	EMBL; AF323757; AAK73366.1; -				
DR	InterPro; IPRO03452; SCF.				
DR	Pfam; PF02404; SCF; 1.				
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion; Alternative splicing.				
KW	SIGNAL	1	25		
FT	CHAIN	26	274		
FT	DOMAIN	26	215		
FT	TRANSMEM	216	238		
FT	DOMAIN	239	274		
FT	DISULFD	29	114		
FT	DISULFD	68	164		
FT	CARBOHYD	90	90		
FT	CARBOHYD	97	97		
FT	CARBOHYD	145	145		
FT	CARBOHYD	196	196		
FT	VASPLIC	175	203		
FT					
FT	/Ptm=VSP_006024.				
FT	S -> P (IN REF. 1; AAK73366).				
FT	S -> N (IN REF. 1; AAK73366).				
FT	EREROEV -> RESFKKNGCFYHTVLSTYLGG (IN REF. 1; AAK73366).				
FT	SEQUENCE	274 AA;	31034 MW;	SACI619014AASE5E72 CRC64;	

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Query Match Similarity      80.4%; Score 1014.5; DB 1; Length 274;
Best Local Similarity      73.7%; Pred. No. 14e-73;
Matches      202; Conservative      20; Mismatches      23; Indels      29; Gaps      2.

QY      1 MKKTQTMILTCIYIQLLLFNLPLVKTEGGCRNRKRVNNVNDVTKLVANLPRDYMTLTKYVP 60
DB      1 MKKTQTMILTCIYIQLLLFNLPLVRKGGCRNRKRVNDVTKLVANLPRDYMTLTKYVP 60

QY      61 MDVLPSCWISBMVVQVSDSLTDLIDKFSNISSEGLSNYSIIDKLVNIYDVLVECKENSS 120
DB      61 MDVLSHCWIRWVQVLSVSLTDLIDKFSNISSEGLSNYSIIDKLVNIYDVLVECKEHS 120

QY      121 KDVKSEFSPEPRVLTPEEPFRIFENRSIDAFDFV-VVASFSDCVVSSSTLSPK----- 174
DB      121 ENVKSSPPNPEPRHAPDFPRIFENRSIDALKDLFTVASKISECVLPSTLSPEKSRVSV 180

QY      175 -----KKNPPGDSLSHMAMALPALFSLIIFGAFGLYMKK 211
DB      181 TKPFLPPVVAASLRLNDSSSNRKAANPLGDSNLQMAALPALFSLVIIGAFGLYMKK 240

QY      212 RPSLTRAVENTIINEEDNEISMLOEKREPEQV 245
DB      241 KQPNLTRAENTIINEEDNEISMLOEKREPEQV 274

RESULT 9
SCF_RAT      STANDARD;      PRT;      273 AA.
ID_P21581; O9QWZ4; O9Z2E7;
AC      01-MAY-1991 (Rel. 18, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Kit ligand precursor (G-Kit ligand) (Stem cell factor) (SCF) (Nast
DE      cell growth factor) (MCF) (Hematopoietic growth factor KL).
DE      KITLG OR MGF.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxId=10116;
RN      [1]
RN      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP      Teramoto T., Nagashima M., Thorngelsson S.S.;
RL      Submitted (JUN-1998) to the EMBL/GenBank/DBS databases.
RN      [2]
RN      SEQUENCE OF 1-201 FROM N.A., AND PARTIAL SEQUENCE.
RP      MEDLINE=91004219; PubMed=2208279;
RA      Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Tung J., Okino K.H.,
RA      Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz E.A., Birckett N.C.,
RA      Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
RA      Fisher E.F., Brjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,
RA      Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zeebo K.M.;
RT      "Primary structure and functional expression of rat and human stem
RT      cell factor DNAs.";
RL      Cell 63:203-211(1990).
RN      [3]
RN      SEQUENCE OF 26-190, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RP      STRAIN=Buffalo; TISSUE=Liver;
RC      MEDLINE=91217037; PubMed=1708771;
RA      Lu H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren S.,
RA      Mendiaz E.A., Zeebo K.M., Langley K.E.;
RT      "Amino acid sequence and post-translational modification of stem cell
RT      factor isolated from buffalo rat liver cell-conditioned medium.";
RL      J. Biol. Chem. 266:8102-8107(1991).
RN      [4]
RN      SEQUENCE OF 26-39.
RP      MEDLINE=91004218; PubMed=2208278;
RA      Zeebo K.M., Wypych J., McNiece I.K., Lu H.S., Smith K.A.,
RA      Kariete S.B., Sachdev R.K., Yuchenkoff V.N., Birckett N.C.,
RA      Williams L.R., Satyagal V.N., Tung W., Bosseman R.A., Mendiaz E.A.,
RA      Langley K.E.;
RT      "Identification, purification, and biological characterization of
RT      hemopoietic stem cell factor from buffalo rat liver-conditioned
RT      medium.";

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[illegible]

OY 175 -----KAKNPPGDSLSHMAALPALFSLIIGFAGALYMKR 212
 DB 181 KPFMLPVAASSLRNDSSSNRAKSPEDPGQWTRMLPALISIVIGFALCALYMKK 240
 OY 213 QPSLTRAVENTIQINEDNEISM/OEKEREFOEV 245
 DB 241 OSSLTRAVENIQINEDNEISM/OEKEREFOEV 273
 RESULT 10
 SCF_MOUSE STANDARD; PRT; 273 AA.
 ID SCF_MOUSE P20826; P97332; Q62524; Q64222; Q921NS;
 AC G1-FEB-1991 (Rel. 17, Created)
 DT G1-MAY-1991 (Rel. 18, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE cell ligand precursor (C-Kit ligand) (stem cell factor) (SCF) (Mast cell growth factor) (MGF) (hematopoietic growth factor KL) (Steel factor).
 GN KITLG OR KITL OR MGF OR SL OR SLF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=MCB6F1.
 RX MEDLINE=91004223; PubMed=1658556;
 RA Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J., Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D., Williams D.E.,
 RT "Molecular cloning of mast cell growth factor, a hematopoietin that is active in both membrane bound and soluble forms.";
 RL Cell 63:235-243(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=92330001; PubMed=1378327;
 RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
 RT "Differential expression and processing of two cell associated forms of the kit-ligand: KL-1 and KL-2.";
 RL Mol. Biol. Cell 3:349-362(1992).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=MCB6F1.
 RX MEDLINE=91160046; PubMed=1705866;
 RA Flanagan J.G., Chan D.C., Leder P.;
 RT "Transmembrane form of the kit ligand growth factor is determined by alternative splicing and is missing in the Slid mutant.";
 RL Cell 64:1025-1035(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=93012940; PubMed=1383087;
 RA Brannan C.L., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A., Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A., Copeland N.G.;
 RT "Developmental abnormalities in Steel^{17H} mice result from a splicing defect in the steel factor cytoplasmic tail.";
 RL Genes Dev. 6:1832-1842(1992).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J;
 RX MEDLINE=97002551; PubMed=884989;
 RA Bedell M.A., Copeland N.G., Jenkins N.A.;
 RT "Multiple pathways for Steel regulation suggested by genomic and sequence analysis of the murine Steel gene.";
 RL Genetics 142:927-934(1996).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS PRO-193 AND SER-207.
 RC STRAIN=C3H/El; TISSUE=Brain;
 RX MEDLINE=97032354; PubMed=8875893;
 RA Graw J., Loetscher J., Neuhäuser-Klaus A., Pretsch W., Schmitt-John T.;
 RT "Molecular analysis of two new Steel mutations in mice shows a transversion or an insertion.";
 RL Mamm. Genome 7:843-846(1996).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS SER-122, PRO-193 AND SER-207.
 RC STRAIN=102/El x C3H/El;
 RX MEDLINE=98025115; PubMed=9360640;
 RA Graw J., Neuhäuser-Klaus A., Pretsch W.;
 RT "Detection of a point mutation (A to G) in exon 5 of the murine Mgf gene defines a novel allele at the Steel locus with a weak phenotype.";
 RL Mutat. Res. 382:75-78(1997).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kanuya M., Lee N.H., Lyons P., Marchionni L., Mashima Y., Mazarelli J., Mombaerts P., Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SER-207.
 RX MEDLINE=22388257; PubMed=12477932.
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshynski S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RP SEQUENCE OF 1-270 FROM N.A. (ISOFORM 1), AND SEQUENCE OF 26-65.
 RX MEDLINE=91004220; PubMed=1698557;
 RA Huang E., Nocka K., Beiler D.R., Chu T.Y., Buck J., Lahm H.W., Wellner D., Leder P., Besmer P.;
 RT "The hematopoietic growth factor KL is encoded by the Sl locus and is the ligand of the c-kit receptor, the gene product of the W locus.";
 RL Cell 63:225-233(1990).
 RN [11]
 RP SEQUENCE OF 1-201 FROM N.A.
 RX MEDLINE=91004220; PubMed=1698556;
 RA Zsebo K.M., Williams D.A., Geisler E.N., Broudy V.C., Martin F.H., Atkins H.L., Hsu R.-Y., Birkett N.C., Okino K.H., Mudrock D.C., Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattarachi B.M.,

RA Gall1 S.J., Suggs S.V.;
 RT "stem cell factor is encoded at the Sl locus of the mouse and is the
 RT ligand for the c-kit tyrosine kinase receptor."
 RL Cell 63:213-224(1990).
 RN [12]
 RP SEQUENCE OF 26-53.
 RX MEDLINE=91004216; PubMed=1698554;
 RA Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A.,
 RA Cosman D., Anderson D., Lyman S.D., Williams D.E.;
 RT "Mast cell growth factor maps near the steel locus on mouse
 RT chromosome 10 and is deleted in a number of steel alleles."
 RL Cell 63:175-183(1990).
 RN [13]
 RP PARTIAL SEQUENCE OF 26-78.
 RX MEDLINE=91004215; PubMed=1698553;
 RA Williams D.E., Eisenman J., Baird A., Rauch C., van Nese K.,
 RA March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S.,
 RA Burgess G.S., Cosman D., Lyman S.D.;
 RT "Identification of a ligand for the c-kit proto-oncogene."
 RL Cell 63:167-174(1990).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins.
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
 CC Also exists as a secreted soluble form (isoform 1 only) (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=KL-1;
 CC IsoId=p20826-1; Sequence=Displayed;
 CC Name=2; Synonyms=KL-2;
 CC IsoId=p20826-2; Sequence=VSP_006023;
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC isoform 1 in the extracellular domain.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M59915; AAA40095.1; -
 CC DR EMBL; M57647; AAA39538.1; -
 CC DR EMBL; S40534; AAB23555.2; -
 CC DR EMBL; X68989; CAA48778.1; -
 CC DR EMBL; U44724; -; NOT ANNOTATED - CDS.
 CC DR EMBL; U44725; AAC52447.1; -
 CC DR EMBL; X95381; CAA64667.1; -
 CC DR EMBL; X99322; CAA67698.1; -
 CC DR EMBL; Y10287; CAA71329.1; -
 CC DR EMBL; AK018777; BAB31402.1; -
 CC DR EMBL; BC011322; AAH11322.1; -
 CC DR EMBL; S40364; AAB23554.2; -
 CC DR EMBL; M59912; AAA39539.1; -
 CC DR PIR; A37934; A37934.
 CC DR PIR; S65801; S65801.
 CC DR MGI; MGI:96974; Kiti1.
 CC DR GO; GO:0016021; C:integral to membrane; IDA.
 CC -----
 CC Query Match 78.5%; Score 991; DB 1; Length 273;
 CC Best Local Similarity 72.2%; Pred. No. 1e-71;
 CC Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;
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 CC QY 1 MKKTQWITICTIYQLLFPNPLVTEGICRRNVTNNVADVTKLVANLPKQWMITLTKYVP 60
 CC DB 1 MKKTQWITICTIYQLLFPNPLVTEGICRRNVTNNVADVTKLVANLPNPNYMITLNVAVG 60

QY 61 MDVLPSCWISWVYVQLSDLTLDLDFGNSISEGHSNYSIIDKLXVNIYDLYECVENGS 120
 DB 61 MDVLPSCWLRMVIQLSLSTLTLDLDFGNSISEGHSNYSIIDKLXVNIYDLYECVENNP 120
 QY 121 KDLKSFKSPPEPLFTPEEFPRIPNRSIDAFQDVVAESTDQVSSSTLSPEKG----- 174
 DB 121 KIKESPKRPFERSFPPEEFPSIFNRSIDAFQDVVAESTDQVSSSTLSGPEKDSRVY 180
 QY 175 ----- KAKNPQDSSLIHMAAMLPLFSLITIGFAGCALYWKRR 212
 DB 181 KPFMLPPVAASSLRNDSSSNRKAAPEDSGLTAMALPALISLVIGFAGCALYWKRR 240
 QY 213 QPSLTAVERNIOINEEDNEISMLQEKERPEFOY 245
 DB 241 QSLTAVERNIOINEEDNEISMLQEKERPEFOY 273
 CC -----
 CC RESULT 11
 CC SCF_SHEEP STANDARD; PRT; 267 AA.
 CC ID P93568; 028591.
 CC AC 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DE 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
 CC cell growth factor) (MGF) (Fragment).
 CC GN KITLG OR SCF.
 CC OS Ovis aries (Sheep).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Caprinae; Ovis.
 CC OX NCBI_Taxid=9940;
 CC RN [1]
 CC RP SEQUENCE OF 8-267 FROM N.A.
 CC RC TISSUE=Ovarian follicle;
 CC RX MEDLINE=96413880; PubMed=8662240;
 CC RA Tisdall D.J., Quirke L.D., Galloway S.M.;
 CC RT "Ovine stem cell factor gene is located within a syntenic group on
 CC chromosome 3 conserved across mammalian species."
 CC RL Mamm. Genome 7:472-473 (1996).
 CC RN [2]
 CC RP SEQUENCE OF 1-202 FROM N.A.
 CC RA McInnes C.J., Logan M., Falconer V.M., Rawlins P., Huntly J., Haig D.;
 CC RT "Molecular cloning and biological activity of ovine stem cell
 CC factor."
 CC RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 CC CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins (By similarity).
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
 CC secreted soluble form (By similarity).
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC the extracellular domain (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U98974; AAB49491.1; -
 CC DR EMBL; Z50743; CAA90620.1; -
 CC DR PIR; S58313; S58313.
 CC DR InterPro; IPR003452; SCF.
 CC DR Pfam; PF02404; SCF_1.
 CC Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.

FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 >267 KIT LIGAND.
FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 POTENTIAL.
FT DOMAIN 239 >267 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 114 BY SIMILARITY.
FT DISULFID 68 164 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 267 267
SQ SEQUENCE 267 AA; 30148 MW; 909D9359E4B9EC841 CRC64;
Query Match 78.5%; Score 990.5; DB 1; Length 267;
Best Local Similarity 74.2%; Pred. No. 1.1e-71;
Matches 198; Conservative 19; Mismatches 21; Indels 29; Gaps 2;
QY 1 MKKTQWILTCIYQLLEFNPVLTGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
1 MKKTQWILTCIYQLLEFNPVLTGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVLTGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
QY 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISGLSNYSIIDLVNIYDDLYECVKENS 120
61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISGLSNYSIIDLVNIYDDLYECVKENS 120
DB 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISGLSNYSIIDLVNIYDDLYECVKENS 120
QY 121 KDLKSEKSPPEPLFTPEEFRIENRSIDAFKDF-VVASETSDCVVSSSTLSPKSG- 174
121 KDLKSEKSPPEPLFTPEEFRIENRSIDAFKDF-VVASETSDCVVSSSTLSPKSG- 174
DB 121 ENVKSSKSPPEPQFTPEKFGIFNKSIDAFKDLFVASTMSCVSISSSTSPKDSRVSV 180
121 ENVKSSKSPPEPQFTPEKFGIFNKSIDAFKDLFVASTMSCVSISSSTSPKDSRVSV 180
QY 175 -----KANNPQDSSILHMAAMALPALFSLIIGFAGALYMK 211
175 -----KANNPQDSSILHMAAMALPALFSLIIGFAGALYMK 211
DB 181 TRKFMPLPVAAASLRNDSSSNRKAISNIDSLSIQNAVALPAFSLVIGFAGALYMK 240
181 TRKFMPLPVAAASLRNDSSSNRKAISNIDSLSIQNAVALPAFSLVIGFAGALYMK 240
QY 212 RQPSLTRAVENTIOINEEDNEISMLOEK 238
212 RQPSLTRAVENTIOINEEDNEISMLOEK 238
DB 241 KQNLTRTVENRQINEEDNEISMLOEK 267
241 KQNLTRTVENRQINEEDNEISMLOEK 267
RESULT 12
SCF_CHICK STANDARD; PRT; 287 AA.
ID SCF_CHICK
AC Q09108;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
GN KITLG OR SCF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OC NCBI_TaxID=9031;
RN NCB1_TaxID=9031;
RX SEQUENCE FROM N.A.
MEDLINE=93273244; PubMed=7684722;
RA Zhou J., Ohtaki M., Sakurai M.;
RT "Sequence of a cDNA encoding chicken stem cell factor.";
RL Gene 127:269-270(1993).
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hemopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).
CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -1- PTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----

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DR EMBL, D13516; BAA0273.1; -;
DR PIR, JN0637; JN0637.
DR InterPro, IPR003452; SCF.
DR Pfam, PF02404; SCF, 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 287 KIT LIGAND.
FT DOMAIN 26 225 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 226 246 POTENTIAL.
FT DOMAIN 247 287 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 117 BY SIMILARITY.
FT DISULFID 68 167 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 287 AA; 32328 MW; 6AE8556ADC152578 CRC64;
Query Match 46.3%; Score 584; DB 1; Length 287;
Best Local Similarity 44.6%; Pred. No. 2.3e-39;
Matches 128; Conservative 46; Mismatches 71; Indels 42; Gaps 7;
QY 1 MKKTQWILTCIYQLLEFNPVLTGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
1 MKKTQWILTCIYQLLEFNPVLTGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVLTGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
QY 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNI-----SEGSNYSIIDLVNIYDDLYECVK 117
61 MDVLPSCWISSENVVQSDSLTDLDFKFSNI-----SEGSNYSIIDLVNIYDDLYECVK 117
DB 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNI-----SEGSNYSIIDLVNIYDDLYECVK 117
QY 118 NSSKD-LKSPKSPPEPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSSTL-SPEKSG 175
118 NSSKD-LKSPKSPPEPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSSTL-SPEKSG 175
DB 121 DKNDPFIENGHLVIEDPFIENPFRILFNSTIEYKERRADSLDKNDCLMPSTVEIPENDS 180
121 DKNDPFIENGHLVIEDPFIENPFRILFNSTIEYKERRADSLDKNDCLMPSTVEIPENDS 180
QY 176 -----AKNPP-----GSSLHMAAMALPALFSLIIG 201
176 -----AKNPP-----GSSLHMAAMALPALFSLIIG 201
DB 181 RVAVTKTSPPPVAAASLRNDISGNTSSNKNKALGFISSSLGSIATLSLILIG 240
181 RVAVTKTSPPPVAAASLRNDISGNTSSNKNKALGFISSSLGSIATLSLILIG 240
QY 202 FAFGLYMKRQPSLTRAVENTIOIN--EEDNEISMLOEKREPEV 245
202 FAFGLYMKRQPSLTRAVENTIOIN--EEDNEISMLOEKREPEV 245
DB 241 FLGALYMKRQPSLTRAVENTIOIN--EEDNEISMLOEKREPEV 287
241 FLGALYMKRQPSLTRAVENTIOIN--EEDNEISMLOEKREPEV 287
RESULT 13
SCF_COTUA STANDARD; PRT; 287 AA.
ID SCF_COTUA
AC Q90314; Q90315;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
GN KITLG OR SCF.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
OC NCBI_TaxID=93934;
RN NCB1_TaxID=93934;
RX SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=96283808; PubMed=8679698;
RA Pectite J.N., Kulik M.J.;
RT "Cloning and characterization of cDNAs encoding two forms of avian stem cell factor.";
RL Biochim. Biophys. Acta 1307:149-151(1996).
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to

CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins (By similarity).
 CC SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
 CC Also exists as a secreted soluble form (isoform 1 only) (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC Name=2;
 CC IsoId=Q09014-1; Sequence=Displayed;
 CC IsoId=Q09014-2; Sequence=VSP 006026;
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC isoform 1 in the extracellular domain.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U43078; AAC59933.1; -;
 CC DR EMBL: U43079; AAC59934.1; -;
 CC DR InterPro: IPR003452; SCF.
 CC DR Pfam: PF02404; SCF; 1.
 CC KM Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
 CC Alternative splicing.
 CC FT SIGNAL 1 25
 CC FT CHAIN 26 287
 CC FT DOMAIN 26 225
 CC FT TRANSMEM 226 246
 CC FT DOMAIN 247 287
 CC FT DISULFID 29 117
 CC FT DISULFID 68 167
 CC FT CARBOHYD 100 100
 CC FT CARBOHYD 106 106
 CC FT CARBOHYD 149 149
 CC FT CARBOHYD 178 178
 CC FT CARBOHYD 200 200
 CC FT CARBOHYD 206 206
 CC FT VARSPPLIC 179 213
 CC
 CC FT POTENTIAL.
 CC KIT LIGAND.
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC DSRVAVTKTSFPVVAASLRNDISGSNTSSNSNK -> E
 CC (in isoform 2).
 CC /FTid=VSP 006026.
 CC /FTid=VSP 006026.
 CC
 CC SO SEQUENCE 287 AA; 32455 MW; ABA81AER422A702E CRC64;
 CC
 CC Query Match 46.2%; Score 583; DB 1; Length 287;
 CC Best Local Similarity 44.3%; Pred. No. 2.8e-39;
 CC Matches 127; Conservative 47; Mismatches 71; Indels 42; Gaps 7;
 CC
 CC 1 MKKTQWILTCYQLLLFNPLVTEGICRNRTNNKDVTKLVANLPKDYMTLTKVPG 60
 CC 1 MKKARQWITITFCQLLLNPLVTKTQSSCGNPTDDVNDIAKLVGNLPNDYITLTKVPR 60
 CC
 CC 61 MDVLPSCWISSEWVQSLDLDLDF--SNISEGLSNYSIIIDKLVNIVDDLVCEVKE 117
 CC 61 MDLSPNHCWILHWPEFSRSLHNLQKFVDISDMSDVLSNYSIINNLTRIINDLMCLAF 120
 CC
 CC 118 NSSKD-LKSKFSKSEPLFLTPEEFRRFNRSIDAFKDFVVASETSDCVSSTL-SPKKK 175
 CC 121 DKNDPFIKENGHLYEEDRFLPENFFRLNRTIEVYKFAASLDPKNDIMPSYETPEPDS 180
 CC
 CC 176 -----AKPP-----GDSSLHMAAMLPALFSLIIG 201
 CC 181 RVAVTKISFPVVAASLRNDISGSNTSSNSNKALGFISSSSLQGISLTLSLILIG 240
 CC
 CC 202 FAFGALYWKGRQP-SLTRAVENIQT--EEDNEISMLQEKEREFOEV 245
 CC 241 FILGVIVYWKTHPKRPSRNSNETTQCHGCGENEISMLQEKEREHLQV 287

RESULT 14
 MURE_WIGBR
 ID MURE_WIGBR STANDARD; PRT; 496 AA.
 AC Q8D2Z1;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE UDP-N-acetylmuramoyl-L-D-glutamate--2,6-diaminopimelate ligase
 DE (EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-
 DE diaminopimelate-adding enzyme) (UDP-MurNac-tripeptide synthetase).
 GN MURE OR WIGBR210.
 OS Wigglesworthia glossinidia brevipalpis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Wigglesworthia.
 OK NCBI_TaxId=36870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22297718; PubMed=12219091;
 RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
 RA Aksoy S.;
 RT Genome sequence of the endocellular obligate symbiont of tsetse
 RT flies, Wigglesworthia glossinidia.";
 RL Nat. Genet. 32:402-407(2002).
 CC -1- FUNCTION: Cell wall formation. Diaminopimelic acid adding enzyme
 CC (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-
 CC glutamate + meso-2,6-diaminoheptanedioate = ADP + phosphate + UDP-
 CC N-acetylmuramoyl-L-alanyl-D-gamma-glutamyl-meso-2,6-diamino-
 CC heptanedioate.
 CC -1- PATHWAY: peptidoglycan biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the murCDB family.
 CC -----
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 CC -----
 CC EMBL: AB063521; BAC24357.1; -;
 CC DR HAMAP, MF_00208; 1.
 CC DR InterPro: IPR005761; Mure.
 CC DR InterPro: IPR00713; Mur_Ligase.
 CC DR InterPro: IPR004101; Mur_Ligase_C.
 CC DR Pfam: PF01225; Mur_Ligase; 1.
 CC DR Pfam: PF02875; Mur_Ligase_C; 1.
 CC DR TIGRfam: TIGR01085; mure; 1.
 CC DR Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
 CC ATP-binding; Complete proteome.
 CC NP BIND 118 124
 CC ATP (POTENTIAL).
 CC
 CC SO SEQUENCE 496 AA; 57220 MW; AB624DA57ADDAC1B CRC64;
 CC
 CC Query Match 7.8%; Score 99; DB 1; Length 496;
 CC Best Local Similarity 21.2%; Pred. No. 1.5;
 CC Matches 50; Conservative 44; Mismatches 78; Indels 64; Gaps 12;
 CC
 CC 1 MKKTQWILTCYQLLL-----FNPL--VKTEGICRNRTNNKDVTKLVANLPRD 50
 CC 154 MKKSKTNTTSAIKCQLLNFPLKKNINIVMEVSSHGLQNNV-NNINFFSAIFSLSD 212
 CC
 CC 51 YMTLLKYVGMVDPVLSHCWISSEWVQSLDLDLDFSNISEGLSNY-SIDK-LVNI 107
 CC 213 -----HIDYHKNMQYEQSKKKLSKL-NVYKIIINVDVIGKMWIKKI 255
 CC
 CC 108 VDDLVCEVENSGLDKSKFSKPERPLRTPEEFRRFNRSIDAFKDFVVASETSDCVS 167
 CC 256 PMSIIVSTKSKIKKFKNL-----KMYVKDIFHYFGTKLS-----ISSWGSVCVINT 303
 CC
 CC 168 TISPEKGAKNPFPGDSLHMAAMLPALFSLIIGFAGALYWKGRQPSLTRAVENI 223

DB 304 KIF-----GEFINNLLSPVAL--LTLGYNF-----KSLANVAENL 338

RESULT 15
T2EA_YEAST STANDARD; PRT; 482 AA.
AC F36100;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transcription initiation factor IIF, alpha subunit (TFII α)
DE (Transcription factor IIF, alpha subunit (TFII α)).
GN TPA1 OR YKL028W.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Bacteria; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 66-71; 102-108 AND 206-220.
RC STRAIN=B926;
RX MEDLINE=95050500; PubMed=7961670;
RA Feaver W.J., Henry N.L., Bushnell D.A., Sayre M.H., Brickner J.H.,
RT Gileadi O., Kornberg R.D.;
RT "Yeast TFII α . Cloning, expression, and homology to vertebrate
RT proteins.";
RL J. Biol. Chem. 269:27549-27553 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Rieger M.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECRUITS TFIIH TO THE INITIATION COMPLEX AND STIMULATES
CC THE RNA POLYMERASE II C-TERMINAL DOMAIN KINASE AND DNA-DEPENDENT
CC ATPASE ACTIVITIES OF TFIIH. BOTH TFIIH AND TFII α ARE REQUIRED FOR
CC PROMOTER CLEARANCE BY RNA POLYMERASE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: BELONGS TO THE TFII α ALPHA SUBUNIT FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U12825; AA62665.1; -;
DR EMBL; Z28028; CA61863.1; -;
DR PIR; S37845; S37845.
DR TRANSFAC; T02239; -;
DR SGD; S0001511; TPA1.
DR InterPro; IPR002853; TFII α .
DR Pfam; PF02002; TFII α .
DR SMART; SM00531; TFII α .
DR Transcription regulation; Nuclear protein; Zinc-finger.
DR Transcription regulation; Nuclear protein; Zinc-finger.
DR Transcription regulation; Nuclear protein; Zinc-finger.
FT ZN FING 124 152 C4-TYPE (POTENTIAL).
FT DOMAIN 374 482 ASP/GLU-RICH (HIGHLY ACIDIC).
FT FT 374 392 POLY-GLU.
SQ SEQUENCE 482 AA; 54742 MW; 3E789DFC4247EF8A CRC64;

Query Match 7.7%; Score 97; DB 1; Length 482;
Best Local Similarity 18.4%; Pred. No. 2.1;
Matches 54; Conservative 53; Mismatches 89; Indels 98; Gaps 11;

QY 12 IYQLLEPLVLTGICNNRVTVNKKVATKLVANIPKDYMITL----- 55
DB 27 LVLDALIFSHVAEDDL-KQLSLINKTEGLPIARLSRDLISIHKOREYPPNSKSVERY 85
QY 56 -----KYVPMGVLPSCW--ISEMNVQLSDSLTD-----LIDKFSNI----- 91
DB 86 YYYVKKYPAIDAK--MKVHOVQRLKDDLDKNSSEPNQWPCICLTXYTQLEAVQLNF 142
QY 92 -----SEGLSNYSIIDKLAVNIIVDLVACV-----KENSCKDLKSKFSKP 130

DB 143 DRTFELCSLCEPLVEDDSGKKKKEKODKLNRIMDOIQIIDSLSKIDDSRIEENTFEIA 202
QY 131 EPRLTPEEFPRIFPFRSIDAPDPPVVASETDCVSSSTLSPKGGAKNPPGDSLSHWMAM 190
DB 203 IARLIPQ-----NOSHAAV-----TYNPKGSTMFRPGDQA----- 234
QY 191 ALPALFSLIGFAGALYMKRQPSLTRAVENTIQINEEDNEISMLOEKEREPQ 244
DB 235 PLPNLMGTALGND-----SRAGANSQATYIHINTTASDVAQRELOERQAE 283

Search completed: February 5, 2004, 15:05:52
Job time : 8.76171 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:59:08 ; Search time 28.6846 Seconds
(Without alignments)
2204.073 Million cell updates/sec

Title: US-09-224-683-63

Perfect score: 1262
Sequence: 1 MKKTQTWITCIYLQLLFPN.....NEEDNEISMLQEKEREFGQEV 245

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPTRMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	715	56.7	208	11	064384
2	509	40.3	123	11	061854
3	480	38.0	160	11	08C9K1
4	339	26.9	271	13	09YGP2
5	286	22.7	270	13	08AVN7
6	145	11.5	36	6	08SPW7
7	128	10.1	1697	5	08IFW4
8	128	10.1	1711	5	08MWP2
9	128	10.1	1713	5	08MWP1
10	128	10.1	1716	5	08MWH2
11	109	8.6	937	10	09MAL4
12	105.5	8.4	1515	5	08IM40
13	102.5	8.1	919	10	09LPD8
14	102.5	8.1	1498	3	096VK6
15	102.5	8.1	1498	3	09P884
16	102	8.1	1501	3	096VL9

17	99	7.8	496	16	08D2Z1	08d2z1 wigleswort
18	99	7.8	539	12	091H18	091h18 discula des
19	97.5	7.7	402	11	035444	035444 mus musculus
20	97	7.7	1447	16	09POJ8	09pqj8 ureaplasma
21	95.5	7.6	1444	5	08ICB9	08icb9 plasmidium
22	94.5	7.5	1515	3	096VK4	096vk4 emericella
23	93.5	7.4	576	11	062970	062970 rattus norv
24	93.5	7.4	647	16	098PP9	098pp9 mycoplasma
25	93.5	7.4	3227	3	013834	013834 schizosacch
26	93	7.4	1298	10	09LSA4	09ls4 arabidopsis
27	93	7.4	1962	10	09FIC2	09fic2 arabidopsis
28	92.5	7.3	335	17	08PXU1	08pxu1 methanobact
29	92.5	7.3	512	16	09CGA7	09cgat lactococcus
30	92.5	7.3	534	5	021299	021299 caenorhabdi
31	92	7.3	420	16	098OM8	098om8 mycoplasma
32	92	7.3	821	16	092RE5	092re5 listeria in
33	91.5	7.3	309	16	08UBA3	08uba3 agrobacteri
34	91.5	7.3	1993	5	P90670	P90670 aplysia cal
35	91.5	7.3	2907	5	08IC71	08ic71 plasmidium
36	91	7.2	281	16	08EUT6	08eut6 mycoplasma
37	91	7.2	317	5	09VTY2	09vty2 drosophila
38	91	7.2	317	5	08SXE8	08sxe8 drosophila
39	90.5	7.2	616	17	026384	026384 methanobact
40	90.5	7.2	774	5	020469	020469 caenorhabdi
41	90.5	7.2	1056	16	08REF7	08ref7 fusobacteri
42	90.5	7.2	1677	12	08V6W0	08v6w0 rice tungro
43	90	7.1	273	11	08C6T7	08c6t7 mus musculu
44	90	7.1	464	16	08EQS0	08eqs0 oceanobacil
45	90	7.1	1218	12	08VAV7	08vav7 white spot

ALIGNMENTS

RESULT 1

064384 PRELIMINARY, PRT, 208 AA.

AC 064384;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Mast cell growth factor (Fragment).
GN KITL OR MGF OR SL OR KL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92330001; PubMed=1378327;
RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
RT "Differential expression and processing of two cell associated forms
of the Kit-1 ligand: KL-1 and KL-2".
RL Mol. Biol. Cell 3:349-362(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160046; PubMed=1705866;
RA Flanagan J.G., Chan D.C., Leder P.;
RT "Transmembrane form of the kit ligand growth factor is determined by
alternative splicing and is missing in the Sld mutant".
RL Cell 64:1025-1035(1991).
DR EMBL, M640536; AAA82556.2; -
DR EMBL, M64262; AAA9378.1; -
DR MGD; MGI:96974; Kitl.
DR InterPro; IPR003452; SCF.
DR Pfam; PFO2404; SCF, 1.
FT NON TER 208
SQ SEQUENCE 208 AA; 23222 MW; C74DD63956EB817 CRC64;

Query Match 56.7%; Score 715; DB 11; Length 208;
Best Local Similarity 79.8%; Pred. No. 3.2e-52;
Matches 138; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

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QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPBHCWISSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPBHCWISSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDLKSKFSPEPRFTPEEFRIENRSIDAFKDFVVASSETSDCVASSTLSPEK 173
DB 121 KNIKESPKRPERSTFPEEFRIENRSIDAFKDFVVASSETSDCVASSTLSPEK 173

RESULT 2
Q61854 PRELIMINARY; PRT; 123 AA.
ID 061854;
AC 061854;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Mast cell growth factor.
GN KITL OR MGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=97032534; PubMed=8875893;
RA Graw J., Loester J., Neuhäuser-Klaus A., Pretsch W., Schmitt-John T.;
RT "Molecular analysis of two new Steel mutations in mice shows a
RT transversion or an insertion."
RL Mamm. Genome 7:843-846 (1996).
DR EMBL: X85379; CA54666.1; -.
DR MGI: 96974; Kitl.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF.
SQ SEQUENCE 123 AA; 13892 MW; A872B4554A85D642 CRC64;

Query Match 40.3%; Score 509; DB 11; Length 123;
Best Local Similarity 81.0%; Pred. No. 3, 2e-35;
Matches 98; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPBHCWISSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPBHCWISSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 K 121
DB 121 K 121

RESULT 3
Q6C9K1 PRELIMINARY; PRT; 160 AA.
ID 06C9K1;
AC 06C9K1;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Kit ligand (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
```

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RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL: AK041961; BAC31113.1; -.
SQ SEQUENCE 160 AA; 17492 MW; B12AC581346AAE6D CRC64;

Query Match 38.0%; Score 480; DB 11; Length 160;
Best Local Similarity 80.7%; Pred. No. 1, 2e-32;
Matches 92; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 6 TWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPGMDVLP 65
DB 46 TWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPGMDVLP 105
QY 66 SHCWISSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 119
DB 106 SHCWISSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 159

RESULT 4
Q9YGP2 PRELIMINARY; PRT; 271 AA.
ID Q9YGP2;
AC Q9YGP2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Steel factor.
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae; Ambystomatidae;
OX NCBI_Taxid=8296;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=99299573; PubMed=10370116;
RA Parichy D.M., Stigson M., Voss S.R.;
RT "Genetic analysis of steel and the pg-M/versican-encoding gene Axxp as
RT candidates for the white (d) pigmentation mutant in the salamander
RT Ambystoma mexicanum."
RL Dev. Genes Evol. 209:349-356 (1999).
DR EMBL: AF119044; AAD17253.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF.
SQ SEQUENCE 271 AA; 30075 MW; 876977ABF7D53EB4 CRC64;

Query Match 26.9%; Score 339; DB 13; Length 271;
Best Local Similarity 35.1%; Pred. No. 1, 6e-20;
Matches 97; Conservative 36; Mismatches 91; Indels 52; Gaps 11;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
QY 57 YVPGMDVLPBHCWISSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVK 116
DB 54 YVPGMDVLPBHCWISSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVK 110
QY 117 -----ENSSKDKSKFSPEPRFTPEEFRIENRSIDAFK-----DFVASSET- 160
DB 111 SGLDNEFFITDPPFDGE---FVPKGFKVTITLLFKAIHGMDDSGTCELPVTTETP 167
QY 161 -SDCVASSTLSPEK-----GKAKNPG-----DS-----SIHMAAMALPALFSLIGFAF 204
DB 168 LSDLPVGTAKSAFSEFWPSSRRKREGIPNAKPDSTSGIALETPTVALISLPSVLGPTI 227
QY 205 GALYWKKROPBLTRAVE---NIQINEDNEISMLQE 237
DB 228 GAVCVKMKHRSKSGCEPTAPCPVRKEAQKSMINQ 263
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RESULT 5
Q8AYN7 PRELIMINARY; PRT; 270 AA.
ID O8AYN7
AC O8AYN7
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Stem cell factor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae, Pipidae;
OC Xenopodidae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Katada T., Yamamoto T., Kitano T., Abe S., Kinoshita T.;
RT "Developmental expression of Xenopus stem cell factor (XSCF).";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB084915; BAC23087.1; -.
SQ SEQUENCE 270 AA; 31017 MW; 462435081000B73A CRC64;

Query Match 22.7%; Score 286; DB 13; Length 270;
Best Local Similarity 29.5%; Pred. No. 4.6e-16;
Matches 81; Conservative 41; Mismatches 99; Indels 54; Gaps 9;

QY 1 MKKTQWILTCIYIQLLF---NPLVTEGICENRVNNYKDVTKLVANLPKQYMITLKY 57
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKKTQWILTCIYIQLLFHGFGRP-----CGNPITDAVNDLPKLVGNIPNDYNNSVRY 53

QY 58 VPGMDVLPBHCWISSEWVQVLSLTLDLKFSNISSEGLSYIIDLKLVNIVDLVCEVKE 117
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 54 VPEKDGLPKHCWLYMMVVEVTHNLDKLSKFEVNTSQ---NVLITKLVSWIFQGIQCIOQL 110

QY 118 NSKDLKSKSEPRFLTEPRFRIRPNRSIDAFK----- 152
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 NDEMDDPSASLYVEIKARDFSVYTSITEVKEINDEYSRLCILPOEYEFVETTED 170

QY 153 DFVASETSDC--VVSSTLSPEKGAKNPQDS---SLHWAAMLPALFSLITGFAGAL 207
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 DFILDSNHDLPVYPSFRKNSRFDSSARSQSGFTGSIQYSTV-LIALACTVIGLGLVL 229

QY 208 -YWKQPSLTRAVENTIINEEDNEISMLQEKERE 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 230 CLKK-----FKHQGTQTDNLGSAVAVPRAE 255

RESULT 6
Q8SPM7 PRELIMINARY; PRT; 36 AA.
ID O8SPM7
AC O8SPM7
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Mast cell growth factor (Fragment).
GN MGF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmutz S.M., Berryere T.G.;
RT "MGF sequencing in the dog aids in mapping to CFAL5.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094360; AAM16279.1; -.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
FT NON_TER 1
FT NON_TER 36
SQ SEQUENCE 36 AA; 4004 MW; D96DD4CF5426F594 CRC64;

Query Match 11.5%; Score 145; DB 6; Length 36;
Best Local Similarity 78.8%; Pred. No. 2.6e-05;

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Matches 26; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 189 AMALPALSILITGFAGALYWKQPSLTRAPE 221
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 SLALPAPFSLVIGFAGALYWKQPSLTRAPE 36

RESULT 7
Q8IFM4 PRELIMINARY; PRT; 1697 AA.
ID O8IFM4
AC O8IFM4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PF0150C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamlin N., Pain A., Berriman B., Hall N., Bowman S., Churcher C.,
RA Harris B., Harris D., Lawson D., Quail M., Barrett B.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035477; CAD49276.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1697 AA; 203378 MW; 0227472866E0B2A CRC64;

Query Match 10.1%; Score 128; DB 5; Length 1697;
Best Local Similarity 21.4%; Pred. No. 0.082;
Matches 52; Conservative 50; Mismatches 85; Indels 56; Gaps 11;

QY 31 NRVTNNVQVTLVAVN-----LPRDNYITLKYVGM-DVLPBHCWISSEWV---Q 76
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1201 HKINNNKDIHTHIVINDNTLOEONRITNEONKIKQIKVSDVPTHINISQOITLNSQ 1260

QY 77 LQSDSLTLDLKFSNISSEGLSN--YSIIDLKLVNIVD--DLVECVKNSKDLKSKSEPRP 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1261 AQNSFENIFMKQONINNDINSKRYVQKITEITINSYDIN-YNKNIKIDYIQQRNIIQ 1319

QY 133 RLFTPEPRFRIRPNRSIDAFKDFVASETSDCVASSTLSPEKGAKN----- 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1320 QNTEITQNLHKININHPKRYFESHQITISV--KNMQEKLKIOEPNKKIQHFKETQI 1377

QY 179 -----PQDSSLHWAAMLPAL---FSLITGFAGALYWKQPSLTRAVENTIINEED 229
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1378 MINKLIQ--SHIHAKMKLPITQOQLMTTL-----HRNEQTKNATRSYNNNEEE 1425

QY 230 NEI 232
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1426 NEM 1428

RESULT 8
Q8MWP2 PRELIMINARY; PRT; 1711 AA.
ID O8MWP2
AC O8MWP2
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Reticulocyte binding protein-like protein 4.
GN RH4.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Indochina III/CDC.
RX MEDLINE=22030722; PubMed=12034462;
RA Kaneo O., Wu J.-B., Tsudoi T., Su X.-Z., Torii M.;
RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
RT protein homologous to the Plasmodium vivax reticulocyte binding
RT proteins.";

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RL Mol. Biochem. Parasitol. 121:275-278(2002).
 DR EMBL: AF420309; AAM47174.1; -
 SQ SEQUENCE 1711 AA; 205236 MW; 254864576A02A5B CRC64;

Query Match 10.1%; Score 128; DB 5; Length 1711;
 Best Local Similarity 21.4%; Pred. No. 0.083;
 Matches 52; Conservative 50; Mismatches 85; Indels 56; Gaps 11;

QY 31 NRVYNNVADVTKLVAN-----LPKDYMITLKYPGM-DVLPSCWISBMV---Q 76
 ID 08MMH2 PRELIMINARY; PRT; 1713 AA.
 AC 08MMH2; 1219 HKINNNLKOITHVINDNNTLOEONRIYNELONKIKQIKNSVDFTHNINYSQILNYSQ 1278
 DB 77 LSDSLTDLDFKNSISEGLSN--YSIIDKLVIYD--DLVECVKENSCKDLKSKFSPSP 132
 QY 1279 AONSFPNIFPMKQINNDINSKRYVQKITEIINSYDIIN-YKNKNIKDIYQGFKNIQ 1337
 DB 133 RLFTPEEFRIFRNSIDAFKDFVVASSETSDCVSSTLSPEKGAKN----- 178
 QY 1338 QLVNTTETQLNHIKONINHFYFESHQITISIV--KNMONEKIKIOEFNKKIOHFKETQI 1395
 DB 179 -----PGDSSIHMAAMALPAL---FSLIIGFAGALYWKRPQSLTRAVENTIQINEED 229
 QY 1396 MINKLIQF--SHIHAKMKLPIYQOQLNTIL-----HRNEQTKNATRSYNNMBEE 1443
 DB 230 NEI 232
 QY 1444 NEM 1446

RESULT 9

Q8MMP1 ID 08MMP1 PRELIMINARY; PRT; 1713 AA.
 AC 08MMP1; 1220 HKINNNLKOITHVINDNNTLOEONRIYNELONKIKQIKNSVDFTHNINYSQILNYSQ 1278
 DB 77 LSDSLTDLDFKNSISEGLSN--YSIIDKLVIYD--DLVECVKENSCKDLKSKFSPSP 132
 QY 1279 AONSFPNIFPMKQINNDINSKRYVQKITEIINSYDIIN-YKNKNIKDIYQGFKNIQ 1337
 DB 133 RLFTPEEFRIFRNSIDAFKDFVVASSETSDCVSSTLSPEKGAKN----- 178
 QY 1338 QLVNTTETQLNHIKONINHFYFESHQITISIV--KNMONEKIKIOEFNKKIOHFKETQI 1395
 DB 179 -----PGDSSIHMAAMALPAL---FSLIIGFAGALYWKRPQSLTRAVENTIQINEED 229
 QY 1396 MINKLIQF--SHIHAKMKLPIYQOQLNTIL-----HRNEQTKNATRSYNNMBEE 1443
 DB 230 NEI 232
 QY 1444 NEM 1446

Query Match 10.1%; Score 128; DB 5; Length 1713;
 Best Local Similarity 21.4%; Pred. No. 0.083;
 Matches 52; Conservative 50; Mismatches 85; Indels 56; Gaps 11;

QY 31 NRVYNNVADVTKLVAN-----LPKDYMITLKYPGM-DVLPSCWISBMV---Q 76
 ID 08MMH2 PRELIMINARY; PRT; 1713 AA.
 AC 08MMH2; 1219 HKINNNLKOITHVINDNNTLOEONRIYNELONKIKQIKNSVDFTHNINYSQILNYSQ 1278
 DB 77 LSDSLTDLDFKNSISEGLSN--YSIIDKLVIYD--DLVECVKENSCKDLKSKFSPSP 132
 QY 1279 AONSFPNIFPMKQINNDINSKRYVQKITEIINSYDIIN-YKNKNIKDIYQGFKNIQ 1337
 DB 133 RLFTPEEFRIFRNSIDAFKDFVVASSETSDCVSSTLSPEKGAKN----- 178
 QY 1338 QLVNTTETQLNHIKONINHFYFESHQITISIV--KNMONEKIKIOEFNKKIOHFKETQI 1395
 DB 179 -----PGDSSIHMAAMALPAL---FSLIIGFAGALYWKRPQSLTRAVENTIQINEED 229
 QY 1396 MINKLIQF--SHIHAKMKLPIYQOQLNTIL-----HRNEQTKNATRSYNNMBEE 1443
 DB 230 NEI 232
 QY 1444 NEM 1446

QY 230 NEI 232
 DB 1448 NEM 1450

RESULT 10

Q8MMH2 ID 08MMH2 PRELIMINARY; PRT; 1716 AA.
 AC 08MMH2; 1220 HKINNNLKOITHVINDNNTLOEONRIYNELONKIKQIKNSVDFTHNINYSQILNYSQ 1278
 DB 77 LSDSLTDLDFKNSISEGLSN--YSIIDKLVIYD--DLVECVKENSCKDLKSKFSPSP 132
 QY 1279 AONSFPNIFPMKQINNDINSKRYVQKITEIINSYDIIN-YKNKNIKDIYQGFKNIQ 1337
 DB 133 RLFTPEEFRIFRNSIDAFKDFVVASSETSDCVSSTLSPEKGAKN----- 178
 QY 1338 QLVNTTETQLNHIKONINHFYFESHQITISIV--KNMONEKIKIOEFNKKIOHFKETQI 1395
 DB 179 -----PGDSSIHMAAMALPAL---FSLIIGFAGALYWKRPQSLTRAVENTIQINEED 229
 QY 1396 MINKLIQF--SHIHAKMKLPIYQOQLNTIL-----HRNEQTKNATRSYNNMBEE 1443
 DB 230 NEI 232
 QY 1445 NEM 1447

Query Match 10.1%; Score 128; DB 5; Length 1716;
 Best Local Similarity 21.4%; Pred. No. 0.083;
 Matches 52; Conservative 50; Mismatches 85; Indels 56; Gaps 11;

QY 31 NRVYNNVADVTKLVAN-----LPKDYMITLKYPGM-DVLPSCWISBMV---Q 76
 ID 08MMH2 PRELIMINARY; PRT; 1716 AA.
 AC 08MMH2; 1220 HKINNNLKOITHVINDNNTLOEONRIYNELONKIKQIKNSVDFTHNINYSQILNYSQ 1278
 DB 77 LSDSLTDLDFKNSISEGLSN--YSIIDKLVIYD--DLVECVKENSCKDLKSKFSPSP 132
 QY 1279 AONSFPNIFPMKQINNDINSKRYVQKITEIINSYDIIN-YKNKNIKDIYQGFKNIQ 1337
 DB 133 RLFTPEEFRIFRNSIDAFKDFVVASSETSDCVSSTLSPEKGAKN----- 178
 QY 1338 QLVNTTETQLNHIKONINHFYFESHQITISIV--KNMONEKIKIOEFNKKIOHFKETQI 1395
 DB 179 -----PGDSSIHMAAMALPAL---FSLIIGFAGALYWKRPQSLTRAVENTIQINEED 229
 QY 1396 MINKLIQF--SHIHAKMKLPIYQOQLNTIL-----HRNEQTKNATRSYNNMBEE 1443
 DB 230 NEI 232
 QY 1445 NEM 1447

RESULT 11

Q9MAL4 ID 09MAL4 PRELIMINARY; PRT; 937 AA.
 AC 09MAL4; 1220 HKINNNLKOITHVINDNNTLOEONRIYNELONKIKQIKNSVDFTHNINYSQILNYSQ 1278
 DB 77 LSDSLTDLDFKNSISEGLSN--YSIIDKLVIYD--DLVECVKENSCKDLKSKFSPSP 132
 QY 1279 AONSFPNIFPMKQINNDINSKRYVQKITEIINSYDIIN-YKNKNIKDIYQGFKNIQ 1337
 DB 133 RLFTPEEFRIFRNSIDAFKDFVVASSETSDCVSSTLSPEKGAKN----- 178
 QY 1338 QLVNTTETQLNHIKONINHFYFESHQITISIV--KNMONEKIKIOEFNKKIOHFKETQI 1395
 DB 179 -----PGDSSIHMAAMALPAL---FSLIIGFAGALYWKRPQSLTRAVENTIQINEED 229
 QY 1396 MINKLIQF--SHIHAKMKLPIYQOQLNTIL-----HRNEQTKNATRSYNNMBEE 1443
 DB 230 NEI 232
 QY 1445 NEM 1447

RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F27F5 from chromosome
 1";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC007915; AAF69150.1; -
 DR InterPro; IPR002713; FF.
 DR InterPro; IPR001005; Myb DNA binding.
 DR InterPro; IPR001202; WW_Reps_WMP.
 DR Pfam; PF01846; FF; 5.
 DR SMART; SM00397; WW; 2.
 DR SMART; SM00441; FF; 4.
 DR SMART; SM00456; WW; 2.
 DR PROSITE; PS00037; MYB_1; 1.
 DR PROSITE; PS50020; WW DOMAIN 2; 2.
 SQ SEQUENCE 937 AA; 107311 MW; 8C8RCDD0641276A62 CRC64;

Query Match 8.6%; Score 109; DB 10; Length 937;
 Best Local Similarity 24.5%; Pred. No. 1.5;
 Matches 59; Conservative 31; Mismatches 99; Indels 52; Gaps 9;

QY 7 WILTCYLLLEPLVKTGICRNRYTNVNDVTK-LVANLEKDYMITLKYPGMDVLP 65
 DB 627 WLDYCIELK-----DLFQYQAVASNTSGSTPKDLFEDVTELEKQYHEDKSYV----- 674

QY 66 SHCWISEMVVQLSDLTDLDFK-SNISGLSNYSIID-KLVNIYDDLVCEVCKENSSKOL 123
 DB 675 -----KDAKMSRKANFKSAISEDLSTQOISDINLKLIYDDLVGRVKEKEKEA 722

QY 124 KKSFKSPERPLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPKGAKNPPGDS 183
 DB 723 RKLQRLAEF-----FTNLLHFTFKEITVNASMED-----SKQVSESSQEVRSIGDE 767

QY 184 SLHWAMALPALSLIIGFAFGALYWKKPSLTRAVENTQIENEDEISMLQEKERFQ 243
 DB 768 SVS-----OGLFEERYI-----TSLQEKAKKERRKDEKVKERKDEKRDOKERR 817

QY 244 E 244
 DB 818 E 818

RESULT 12

OSIM40
 ID OSIM40 PRELIMINARY; PRT; 1515 AA.
 AC OSIM40;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein, conserved.
 DE Pf14.0051.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OC NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3D7;
 RX MEDLINE=22255705; PubMed=12358864;
 RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Paten A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyte S.,
 RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
 RA Petrea M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McRadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.;
 RT "Genome sequence of the human malaria parasite Plasmodium
 falciparum";
 RT Nature 419:498-511(2002).
 RL EMBL; AE014816; AAN36663.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 1515 AA; 179830 MW; 6E5EA9823B80A006 CRC64;

Query Match 8.4%; Score 105.5; DB 5; Length 1515;
 Best Local Similarity 21.3%; Pred. No. 5.5;
 Matches 61; Conservative 48; Mismatches 101; Indels 77; Gaps 13;

QY 8 ILTCI-----YQLLFPNPLVTBEGICNRNRYTNVNDVTKLVANLPK-----DYMITLK 56
 DB 685 VINCIRNRYDFSILVAFVNLN-----QNSFPLNIIKFEELLMNIQKIMKNDLGLFSK 739

QY 57 YVPGMDVLP-----PSHCWISEMVV-----QLSDLTDLDFKSNISGLSNYSI 100
 DB 740 FSYQSDIQAFNDPVIYHENDVNIINELKITEENKLEKSRDLNNTI-----ISNISE 793

QY 101 IRL-----VNIVDLVECVCKENSSKDKLKSFKSPERPLFTPEEFRIFNRSIDAFKDF 154
 DB 794 CKTKRNYNDILNKLITIDNANDIIGIRKNIQKKKNNEQISDFEHLNKKSDVMKTL 853

QY 155 VVASSETSDCVSSTLSPKGAKN-----NPPGDSLHWAMALPALFSLIIGF-AF 204
 DB 854 YTDQVQNKIKTYLFSIYKKKKINEIHNINIQSSSVH-----ILSFVSNFLQIT 905

QY 205 GALY-----WKKRQPSLTRAVENTQIENEDEISMLQEK 238
 DB 906 QALYHNTTSLKKGMS--LPICKHLISYENMSFNNIDKLAYIQK 950

RESULT 13

OS9LPD8
 ID OS9LPD8 PRELIMINARY; PRT; 919 AA.
 AC OS9LPD8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE T12C22.20 protein.
 GN T12C22.20.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Liu S., Vaysberg M., Sakano H., Lee J., Lenz C., Pham P., Toriumi M.,
 RA Yu G., Chin C., Chou J., Choi E., Chung M., Gonzalez A., Hong B.,
 RA Liu A., Alcafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.,
 RA Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 RA Nguyen M., Palm C., Shinn P., Southwick A., Davis R., Ecker J.,
 RA Federspiel N., Theologis A.;
 RT "The sequence of BAC T12C22 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC020576; AAF78276.1; -
 DR InterPro; IPR001005; Myb DNA binding.
 DR InterPro; IPR002713; FF.
 DR InterPro; IPR001202; WW_Reps_WMP.
 DR Pfam; PF01846; FF; 4.
 DR Pfam; PF00397; WW; 2.
 DR SMART; SM00441; FF; 4.
 DR SMART; SM00456; WW; 2.
 DR PROSITE; PS00037; MYB_1; 1.
 DR PROSITE; PS50020; WW DOMAIN 2; 2.
 SQ SEQUENCE 919 AA; 104903 MW; AAF729850A28B61E CRC64;

Query Match 8.1%; Score 102.5; DB 10; Length 919;
 Best Local Similarity 28.0%; Pred. No. 5.3;
 Matches 49; Conservative 24; Mismatches 75; Indels 27; Gaps 6;

QY 72 EMVVOQSDLTDLDFK-SNISGLSNYSIID-KLVNIYDDLVCEVCKENSSDKLKSFKS 129
 DB 651 ELKQISWVSWLFEFKSAISEDLSTQOISDINLKLIYDDLVGRVKEKEKEARLQRL 710

QY 130 PEPRFLTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPKGAKNPPGDSLHWMA 189

Db 711 ABE-----FTNLHTEKEITVASWED-----SKQVBESEQVRSIGDESVS--- 752
QY 190 MALPALFSLIIGFAGALYKKRPSITRAVENIOINEEDNEISMLOEKEREPQ 244
Db 753 ----QGLFEERY-----TSLQEKAKERKRDEKVRKREKDEKXKDKKRE 800

RESULT 14

Q96VK6 PRELIMINARY; PRT; 1498 AA.

AC Q96VK6; 19, Created)
DT C1-DEC-2001 (TREMBlrel. 19, last sequence update)
DT C1-MAR-2003 (TREMBlrel. 23, last annotation update)
DE ABC transporter protein.
GN ATRE.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eucotiales; Trichocomaceae; Emericella.
OX NCB1_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG096;
RA Andrade A.C., Braam C., Haas H., De Waard M.A.;
RT "ABC transporters and resistance to azole fungicides in the ima
RT mutants of Aspergillus nidulans."
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AJ309280; CAC42216.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR000847; HTH_LYR.
DR InterPro; IPR001063; Ribosomal_L22.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
DR PROSITE; PS00044; HTH_LYR_FAMILY; 1.
DR PROSITE; PS00464; RIBOSOMAL_L22; 1.
KW ATP-binding; Transport.
SQ SEQUENCE 1498 AA; 167675 MW; BBE9FF3F46110FEB CRC64;

Query Match 8.1%; Score 102.5; DB 3; Length 1498;
Best Local Similarity 19.6%; Pred. No. 9.7;
Matches 56; Conservative 38; Mismatches 92; Indels 99; Gaps 10;

QY 17 LLENPLVKT-----EGICNRVTNNVQDYTKLVANLPKDYITLK-----YVPG----- 60
Db 263 LMFSLARAPRNRLEGVSRKQYAEHRDV--VMAMLGSHNTINRVGNDPIRGVSGGERK 320
QY 61 -----MDVLPSCHWIS-----MVVQLSDSLTD 83
Db 321 RVSIABEATLSQAPLQCMWNSRGLDSANALEFCCKNALMSKTYGSTACVAITYQASQAYD 380
QY 84 LLDKFSNISSEGLSNY--SIIDKLVINIVDDIVECVKENSXDKLKKFSPEPLRF----- 135
Db 381 VEDKVTLYLEGROIYFGNTKDAKKFVDMGFECEPERQTADPLTSLTSPAERLVRPVEG 440
QY 136 ----TPPEFRIFNRSIDAFK-----DFVVASETSDCVSSTLSPE-KGAKNPP 180
Db 441 RVPCPTPEFAAMWKRSEERAKLMAIEEYEROYPICGSPSYDAFVDARKAMQSKRQVNSP 500
QY 181 -----GDSLSHMAWALPALFSLIIGFAF 204
Db 501 YTISIMQOVSLCVVRGFORLGRDPSLTSTLIGNFMALITIGSVF 545

RESULT 15

Q9P884 PRELIMINARY; PRT; 1498 AA.

AC Q9P884; 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE ABC transporter protein.
GN ATRE.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eucotiales; Trichocomaceae; Emericella.
OX NCB1_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG096;
RA Andrade A.C., Van Nistelrooy J.G.M., Haas H., De Waard M.A.;
RT "ABC transporters and resistance to azole fungicides in the ima
RT mutants of Aspergillus nidulans."
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AJ276241; CAB76823.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR000847; HTH_LYR.
DR InterPro; IPR001063; Ribosomal_L22.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
DR PROSITE; PS00044; HTH_LYR_FAMILY; 1.
DR PROSITE; PS00464; RIBOSOMAL_L22; 1.
KW ATP-binding; Transport.
SQ SEQUENCE 1498 AA; 167706 MW; AABDEA3FPDIAERB CRC64;

Query Match 8.1%; Score 102.5; DB 3; Length 1498;
Best Local Similarity 19.6%; Pred. No. 9.7;
Matches 56; Conservative 38; Mismatches 92; Indels 99; Gaps 10;

QY 17 LLENPLVKT-----EGICNRVTNNVQDYTKLVANLPKDYITLK-----YVPG----- 60
Db 263 LMFSLARAPRNRLEGVSRKQYAEHRDV--VMAMLGSHNTINRVGNDPIRGVSGGERK 320
QY 61 -----MDVLPSCHWIS-----MVVQLSDSLTD 83
Db 321 RVSIABEATLSQAPLQCMWNSRGLDSANALEFCCKNALMSKTYGSTACVAITYQASQAYD 380
QY 84 LLDKFSNISSEGLSNY--SIIDKLVINIVDDIVECVKENSXDKLKKFSPEPLRF----- 135
Db 381 VEDKVTLYLEGROIYFGNTKDAKKFVDMGFECEPERQTADPLTSLTSPAERLVRPVEG 440
QY 136 ----TPPEFRIFNRSIDAFK-----DFVVASETSDCVSSTLSPE-KGAKNPP 180
Db 441 RVPCPTPEFAAMWKRSEERAKLMAIEEYEROYPICGSPSYDAFVDARKAMQSKRQVNSP 500
QY 181 -----GDSLSHMAWALPALFSLIIGFAF 204
Db 501 YTISIMQOVSLCVVRGFORLGRDPSLTSTLIGNFMALITIGSVF 545

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